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OM protein - protein search, using sw model

Run on: December 10, 2003, 20:25:06 ; Search time 11 seconds  
(without alignments)  
115.429 Million cell updates/sec

Title: US-09-936-885-3  
Perfect score: 128  
Sequence: 1 DVLKKGITVALHACKAALGAVADTISQ 27

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues  
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	128	100.0	78	1 DMS1_PHYBI	P80282 phylomedusa
2	110	85.9	34	1 DMS1_PHYSA	P24302 phylomedusa
3	105	82.0	34	1 DMS2_PHYSA	P80278 phylomedusa
4	60.5	47.3	77	1 DRG2_PHYBI	Q902k5 phylomedusa
5	55.5	43.4	76	1 DMS4_PHYBI	P81486 phylomedusa
6	53.5	41.8	81	1 DMS2_PHYBI	P31107 phylomedusa
7	52.5	41.0	81	1 DRG1_PHYBI	Q902k3 phylomedusa
8	51.5	40.2	75	1 DMS2_PACDA	Q93452 pachymedusa
9	51.5	40.2	506	1 ATP0_BETU	Q06735 beta vulgar
10	51.5	40.2	507	1 ATP0_PEA	P05493 plasma sativ
11	51.5	40.2	508	1 ATP0_MAIZE	P05494 zea mays (m
12	51.5	40.2	508	1 ATP0_PHAVU	P24459 phaseolus v
13	51.5	40.2	508	1 ATP0_SOYEN	Q01915 glycine max
14	51.5	40.2	509	1 ATP0_ORYGA	P15998 oryza sativ
15	51.5	40.2	509	1 ATP0_WHEAT	P12862 triticum ae
16	51.5	40.2	510	1 ATP0_HELAN	P18260 helianthus
17	51	39.8	334	1 RUVB_THEMA	Q56313 thermotoga
18	50.5	39.5	507	1 ATP0_ARATH	P92549 arabidopsis
19	50.5	39.5	507	1 ATP0_BRANA	P22201 brassica na
20	50.5	39.5	507	1 ATP0_RAPSA	P23413 rapanus sa
21	50	39.1	71	1 CER1_CERCA	P36190 ceratitidis c
22	50	39.1	71	1 CER2_CERCA	O17512 ceratitidis c
23	50	39.1	75	1 DMS3_AGRAN	Q93223 agalychnis
24	50	39.1	144	1 MAX4_BOMMX	P83083 bombyx max
25	50	39.1	417	1 YEIM_HABIN	P47472 haemophilus
26	49.5	38.7	509	1 ATP0_NICPL	P05495 nicotiana p
27	48.5	37.9	30	1 DMS3_PHYSA	P80279 phylomedusa
28	48.5	37.9	80	1 DMS3_PACDA	Q93453 pachymedusa
29	48.5	37.9	511	1 ATP0_OENBI	P05492 oenothera b
30	48	37.5	495	1 MURE_XILFA	Q9pf85 xyliella fas
31	47	36.7	403	1 CRE4_PSEPU	P38488 pseudomonas
32	47	36.7	697	1 SYGB_RALSO	Q8Y213 ralstonia s
33	46	35.9	71	1 CERD_CERCA	O17513 ceratitidis c

#### ALIGNMENTS

##### RESULT 1

ID	DMS1_PHYBI	STANDARD;	PRT;	78 AA.
AC	P80282;			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Dermaseptin Bi precursor (Dermaseptin Bi).			
OS	Phylomedusa bicolor (Two-colored leaf frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;			
OC	Phylomedusinae; Phylomedusa.			
OX	NCBI_TaxID=8393;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Skin;			
EX	MEDLINE=94299491; PubMed=8074751;			
RA	Amiche M., Ducancel F., Mor A., Boulain J.C., Mensz A., Nicolas P.;			
RT	"Precursors of vertebrate peptide antibiotics dermaseptin b and			
RT	adenoregulin have extensive sequence identities with precursors of			
RT	oid peptides dermorphin, dermenkephalin, and deltorphins.";			
RL	J. Biol. Chem. 269:17847-17853(1994).			
RN	(2)			
RP	SEQUENCE OF 45-75.			
RC	TISSUE=Skin secretion;			
EX	MEDLINE=94139686; PubMed=8306981;			
RA	Mor A., Nicolas P.;			
RT	"Isolation and structure of novel defensive peptides from frog skin.";			
RL	Eur. J. Biochem. 219:145-154(1994).			
CC	- FUNCTION: POSSESSES A POTENT ANTIMICROBIAL ACTIVITY AGAINST			
CC	BACTERIA FUNGI AND PROTOZOA. PROBABLY ACTS BY DISTURBING MEMBRANE			
CC	FUNCTIONS WITH ITS AMPHIPATHIC STRUCTURE.			
CC	- SUBCELLULAR LOCATION: Secreted.			
CC	- TISSUE SPECIFICITY: Skin.			
CC	- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.			
CC	Dermaseptin subfamily.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	or send an email to license@isb-sib.ch).			
CC	EMBL; X73387; CAA51080.1; -			
DR	PIR; A53727; A53727.			
DR	PIR; B54897; B54897.			
DR	InterPro; IPR004275; Brevenin.			
DR	Pfam; PF03032; Brevenin, 1.			
KW	Amphibian defense peptide; Antibiotic; Fungicide; Multigene family;			
FT	SIGNAL; Cleavage on pair of basic residues; Amidation.			
FT	SIGNAL 1 22 POTENTIAL.			
FT	PROPEP 23 42			
FT	CHAIN 45 75			
FT	PROPEP 76 78			
FT	DERMASEPTIN BI.			

P08155 drosophila  
P26854 marchantia  
Q17313 ceratitidis c  
P96910 mycobacteri  
Q43714 gossypium a  
Q8xd64 escherichia  
Q46814 escherichia  
P93736 arabidopsis  
O93224 agalychnis  
P81485 phylomedusa  
Q9rnus streptomyce  
P36191 ceratitidis c

```

FT MOD_RES 75 75 AMIDATION (G-75 PROVIDE AMIDE GROUP)
SQ SEQUENCE 78 AA; 8707 MW; EB3B6F03058FEC6F CRC64;
Query Match 100.0%; Score 128; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 4.1e-11;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVKKIGTVALHAGKAALGAVADTISQ 27
   :|||:|||||:|||||:|||||:|||||:
Db 49 DVKKIGTVALHAGKAALGAVADTISQ 75

RESULT 2
DMS1_PHYSA STANDARD; PRT; 34 AA.
ID DMS1_PHYSA
AC P24302; P80277;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Dermaseptin 1 (DS I).
OS Phyllomedusa sauvegei (Sauvage's leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Phyllomedusinae; Phyllomedusa.
OX NCBI_TaxID=8395;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion; PubMed:1909573;
RX MEDLINE=91363376; PubMed:1909573;
RA Mor A., Nguyen V.H., Delfour A., Migliore-Samour D., Nicolas P.;
RT "Isolation and structure of novel defensive peptides from frog skin.";
RL novel antimicrobial peptide of amphibian skin.";
RL Biochemistry 30:8824-8830(1991).
RN [2]
RP SEQUENCE.
RC TISSUE=Skin secretion; PubMed:8306981;
RX MEDLINE=94139686; PubMed:8306981;
RA Mor A., Nicolas P.;
RT "Isolation and structure of novel defensive peptides from frog skin.";
RL Eur. J. Biochem. 219:145-154(1994).
CC -|- FUNCTION: POSSESSES A POTENT ANTIMICROBIAL ACTIVITY AGAINST
CC BACTERIA FUNGI AND PROTOZOA. PROBABLY ACTS BY DISTURBING MEMBRANE
CC FUNCTIONS WITH ITS AMPHIPATIC STRUCTURE.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Skin.
CC -|- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
KW Amphibian defense peptide; Antibiotic; Fungicide; Multigene family.
SQ SEQUENCE 34 AA; 3455 MW; E2D8CBDSBAC2E40 CRC64;

Query Match 85.9%; Score 110; DB 1; Length 34;
Best Local Similarity 84.6%; Pred. No. 6.2e-09;
Matches 22; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VLKKGITVALHAGKAALGAVADTISQ 27
   :|||:|||||:|||||:|||||:|||||:
Db 6 MLKKGITVALHAGKAALGAAADTISQ 31

RESULT 3
DMS2_PHYSA STANDARD; PRT; 34 AA.
ID DMS2_PHYSA
AC P80278;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Dermaseptin 2 (DS II).
OS Phyllomedusa sauvegei (Sauvage's leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Phyllomedusinae; Phyllomedusa.
OX NCBI_TaxID=8395;

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RN SEQUENCE.
RP TISSUE=Skin secretion; PubMed:8306981;
RX MEDLINE=94139686; PubMed:8306981;
RA Mor A., Nicolas P.;
RT "Isolation and structure of novel defensive peptides from frog skin.";
RL Eur. J. Biochem. 219:145-154(1994).
CC -|- FUNCTION: POSSESSES A POTENT ANTIMICROBIAL ACTIVITY AGAINST
CC BACTERIA FUNGI AND PROTOZOA. PROBABLY ACTS BY DISTURBING MEMBRANE
CC FUNCTIONS WITH ITS AMPHIPATIC STRUCTURE.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Skin.
CC -|- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
KW Amphibian defense peptide; Antibiotic; Fungicide; Multigene family.
SQ SEQUENCE 34 AA; 3473 MW; C528CBDSBAC239E CRC64;

Query Match 82.0%; Score 105; DB 1; Length 34;
Best Local Similarity 80.8%; Pred. No. 3.1e-08;
Matches 21; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 VLKKGITVALHAGKAALGAVADTISQ 27
   :|||:|||||:|||||:|||||:|||||:
Db 6 MLKKGITVALHAGKAALGAAADTISQ 31

RESULT 4
DRG2_PHYSA STANDARD; PRT; 77 AA.
ID DRG2_PHYSA
AC Q90ZK5;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Dermaseptin DRG2 precursor (Dermaseptin 2).
GN DRG2.
OS Phyllomedusa bicolor (Two-colored leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Phyllomedusinae; Phyllomedusa.
OX NCBI_TaxID=8393;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Amiche M.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -|- FUNCTION: Has antimicrobial activity (Potential).
CC -|- SUBCELLULAR LOCATION: Secreted (Probable).
CC -|- TISSUE SPECIFICITY: Skin.
CC -|- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
KW Dermaseptin subfamily.
SQ SEQUENCE.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AJ312001; CAC37580.1; -
CC InterPro; IPR004275; Brevenin.
CC Pfam; PF03032; Brevenin.1
CC Amphibian defense peptide; Antibiotic; Multigene family;
CC Cleavage on pair of basic residues; Amidation; Signal.
KW SIGNAL.
FT PROPEP 1 22 POTENTIAL.
FT PEPTIDE 23 43 POTENTIAL.
FT PROPEP 45 74 DERMASEPTIN DRG2.
FT MOD_RES 74 74
FT AMIDATION (G-75 PROVIDE AMIDE GROUP)
FT (POTENTIAL).
SQ SEQUENCE 77 AA; 8417 MW; 8566BBF7F7A94E55 CRC64;

Query Match 47.3%; Score 60.5; DB 1; Length 77;

```

Best Local Similarity 53.8%; Pred. No. 0.092; Matches 14; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 3 LKKGITVAL-HAGKAALGAVADTISQ 27  
DB 51 IKEAGKAALTAAGKAALGAVSDAVE 76

RESULT 5  
DMS4\_PHYBI STANDARD; PRT; 76 AA.  
AC P81486;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 15-OCT-2001 (Rel. 40, Last sequence update)  
DE Dermaseptin BIV precursor (Dermaseptin B4)  
OS Phyllomedusa bicolor (Two-colored leaf frog)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Phyllomedusinae; Phyllomedusa.  
NCBI\_TaxID=8393;  
RN [1]

SEQUENCE FROM N.A., SEQUENCE OF 46-73, AND MASS SPECTROMETRY.  
RP TISSUE=Skin secretion;  
RX MEDLINE=98278974; PubMed=9614066;  
RA Charpentier S., Amiche M., Mester J., Vouille V., Le Caer J.-P.,  
RA Nicolas P., Delfour A.;  
RT "Structure, synthesis, and molecular cloning of dermaseptins B, a  
RT family of skin peptide antibiotics";  
RL J. Biol. Chem. 273:14690-14697(1998).  
CC -!- FUNCTION: POSSESSES A POTENT ANTIMICROBIAL ACTIVITY AGAINST GRAM-  
CC POSITIVE AND GRAM-NEGATIVE BACTERIA. PROBABLY ACTS BY DISTURBING  
CC MEMBRANE FUNCTIONS WITH ITS AMPHIPATHIC STRUCTURE.  
CC -!- SUBCELLULAR LOCATION: Skin.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- MASS SPECTROMETRY: MW=2997.15; MW ERR=0.1; METHOD=Electrospray.  
CC -!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.  
CC Dermaseptin subfamily.

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EMBL: Y16565; CAA76289.1;  
DR InterPro; IPR004275; Brevinin.  
DR Pfam; PF03032; Brevinin, 1.  
KW Amphibian defense peptide; Antibiotic; Multigene family; Signal;  
KX Cleavage on pair of basic residues; Amidation.  
FT SIGNAL 1 22 POTENTIAL.  
FT PROPEP 23 43  
FT CHAIN 46 73 DERMASEPTIN BIV.  
FT PROPEP 75 76 POTENTIAL.  
FT MOD RES 73 73  
SQ SEQUENCE 76 AA; 8642 MW; A8A0525P0709F447 CRC64;

Query Match 43.4%; Score 55.5; DB 1; Length 76;  
Best Local Similarity 44.4%; Pred. No. 0.45;  
Matches 12; Conservative 4; Mismatches 8; Indels 3; Gaps 1;

QY 1 DVLKKGITVALHAGKAALGAVADTISQ 27  
DB 50 DLKKNVGRK---AGRAVLNTVTDWNVQ 73

RESULT 6  
DMS2\_PHYBI STANDARD; PRT; 81 AA.  
AC P31107; P80283;  
DT 01-JUL-1993 (Rel. 26, Created)

01-OCT-1994 (Rel. 30, Last sequence update)  
15-SEP-2003 (Rel. 42, Last annotation update)  
DE Adenoregulin precursor (Dermaseptin B1) (Dermaseptin B2).  
OS Phyllomedusa bicolor (Two-colored leaf frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Phyllomedusinae; Phyllomedusa.  
NCBI\_TaxID=8393;  
RN [1]

SEQUENCE FROM N.A.  
RP TISSUE=Skin;  
RX MEDLINE=93221546; PubMed=8466537;  
RA Amiche M., Ducancel F., Lajeunesse E., Boulain J.-C., Menez A.,  
RA Nicolas P.;  
RT "Molecular cloning of a cDNA encoding the precursor of adenoregulin  
RT from frog skin. Relationships with the vertebrate defensive peptides,  
RT dermaseptins";  
RL Biochem. Biophys. Res. Commun. 191:983-990(1993).  
RN [2]

SEQUENCE OF 46-78.  
RP TISSUE=Skin secretion;  
RX MEDLINE=93066363; PubMed=1438301;  
RA Daly J.W., Caceres J., Moni R.W., Gusovsky F., Moos M. Jr.,  
RA Seamon K.B., Milton K., Myers C.W.;  
RT "Frog secretions and hunting magic in the upper Amazon:  
RT identification of a peptide that interacts with an adenosine  
RT receptor";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:10960-10963(1992).  
RN [3]

SYNTHESIS, AND CHARACTERIZATION.  
RP TISSUE=Skin;  
RX MEDLINE=94139686; PubMed=8306981;  
RA Mor A., Nicolas P.;  
RT "Isolation and structure of novel defensive peptides from frog skin.";  
RL Eur. J. Biochem. 219:145-154(1994).  
CC -!- FUNCTION: ENHANCES BINDING OF AGONISTS TO A1 ADENOSINE RECEPTORS.  
CC -!- FUNCTION: POSSESSES A POTENT ANTIMICROBIAL ACTIVITY AGAINST  
CC BACTERIA, FUNGI AND PROTOZOA. PROBABLY ACTS BY DISTURBING MEMBRANE  
CC FUNCTIONS WITH ITS AMPHIPATHIC STRUCTURE.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- DISEASE: AFFECTS HUMAN BEHAVIOR ELICITING PROFOUND MALAISE,  
CC FOLLOWED BY LISTLESSNESS AND THEN EUPHORIA.  
CC -!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.  
CC Dermaseptin subfamily.

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EMBL: X70278; CAA49763.1;  
DR PIR; JN0462; JN0462.  
DR InterPro; IPR004275; Brevinin.  
DR Pfam; PF03032; Brevinin, 1.  
KW Amphibian defense peptide; Antibiotic; Fungicide; Multigene family;  
KX Signal; Cleavage on pair of basic residues.  
FT SIGNAL 1 22 POTENTIAL.  
FT PROPEP 23 43  
FT CHAIN 46 78 ADENOREGULIN.  
FT PROPEP 79 81  
SQ SEQUENCE 81 AA; 8844 MW; C26ADB4E9418272D CRC64;

Query Match 41.8%; Score 53.5; DB 1; Length 81;  
Best Local Similarity 40.0%; Pred. No. 0.9;  
Matches 12; Conservative 7; Mismatches 6; Indels 5; Gaps 1;

QY 3 LKKGITVALHAGKAALGAVADTISQ 27  
DB 51 IKEVGKEAKAAKAAKGAALGAVSEAVE 80

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RESULT 7
DRG1_PHYBI
ID DRG1_PHYBI STANDARD; PRT; 81 AA.
AC Q902K3;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Dermaseptin DRG1 precursor (Dermaseptin 1).
GN DRG1.
OS Phyllomedusa bicolor (Two-colored leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Phyllomedusinae; Phyllomedusa.
OX NCBI_TaxID=8393;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Skin;
RC Amiche M.;
RA Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RL -1- FUNCTION: Has antimicrobial activity (Potential).
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
CC Dermaseptin subfamily.
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EMBL; AJ312003; CAG37582.1; -
InterPro: IPR004275; Brevenin; 1.
Pfam: PF03032; Brevenin; 1.
KW Amphibian defense peptide; Antibiotic; Multigene family;
KX Cleavage on pair of basic residues; Amidation; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT PROPEP 23 44 DERMASEPTIN DRG1.
FT PEPTIDE 46 78
FT PROPEP 80 81
FT MOD_RES 78 78
FT FT
FT FT
SQ SEQUENCE 81 AA; 8756 MW; B4B1B984756F8229 CRC64;
Query Match 41.08; Score 52.5; DB 1; Length 81;
Best Local Similarity 52.04; Pred. No. 1.2;
Matches 13; Conservative 3; Mismatches 8; Indels 1; Gaps 1;
OY 4 KKIGTVALH-AGKAALGAVADTISQ 27
DB 56 KEAKAALKAAGKALGAVTDVGE 80
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RESULT 8
DMS2_PACDA
ID DMS2_PACDA STANDARD; PRT; 75 AA.
AC Q93452;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Dermaseptin PD-2-2 precursor.
OS Phyllomedusa dactylos (Giant mexican leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Phyllomedusinae; Pachymedusa.
OX NCBI_TaxID=75988;
[1]
RN SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RP TISSUE=Skin;
RC

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RX MEDLINE=98449786; PubMed=9774745;
RA Wechselberger C.;
RL "Cloning of cDNAs encoding new peptides of the dermaseptin-family.";
CC Biochim Biophys Acta 1388:279-283(1998).
CC -1- FUNCTION: POSSESSES A POTENT ANTIMICROBIAL ACTIVITY AGAINST GRAM-
CC POSITIVE AND GRAM-NEGATIVE BACTERIA. PROBABLY ACTS BY DISTURBING
CC MEMBRANE FUNCTIONS WITH ITS AMPHIPATHIC STRUCTURE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
CC Dermaseptin subfamily.
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-----
EMBL; AJ005190; CAA06427.1; -
InterPro: IPR004275; Brevenin; 1.
Pfam: PF03032; Brevenin; 1.
KW Amphibian defense peptide; Antibiotic; Multigene family;
KX Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT PROPEP 23 42
FT CHAIN 45 75 DERMASEPTIN PD-2-2.
FT SEQUENCE 75 AA; 8508 MW; 6278A607F0B02725 CRC64;
Query Match 40.24; Score 51.5; DB 1; Length 75;
Best Local Similarity 50.04; Pred. No. 1.6;
Matches 13; Conservative 4; Mismatches 6; Indels 3; Gaps 1;
OY 2 VLKIGTVALHAGKAALGAVADTISQ 27
DB 50 LLKKVGKV---AGKAVLNVAVTNMANQ 72
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RESULT 9
ATP0_BETVU
ID ATP0_BETVU STANDARD; PRT; 506 AA.
AC Q06735;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ATP synthase alpha chain, mitochondrial (EC 3.6.3.14).
GN ATPA.
OS Beta vulgaris (sugar beet).
OG Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Chenopodiaceae; Beta.
OX NCBI_TaxID=161934;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=93365027; PubMed=8358823;
RA Senda M., Mikami T., Kinoshita T.;
RL "The sugar beet mitochondrial gene for the ATPase alpha-subunit:
RT sequence, transcription and rearrangements in cytoplasmic
RT male-sterile plants.";
RL Curr. Genet. 24:164-170(1993).
CC -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC GRADIENT ACROSS THE MEMBRANE. THE ALPHA CHAIN IS A REGULATORY
CC SUBUNIT.
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
CC H(+) (Out).
CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC HAS THREE MAIN SUBUNITS: A, B AND C.
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
CC -1- SIMILARITY: Belongs to the ATPase alpha/beta chains family.

```

OC "Nucleotide sequence of the F1-ATPase alpha subunit from maize  
RA [1]  
RP NCB1\_TaxID=4577;  
RX [1]  
PA SEQUENCE FROM N.A.  
PC Braun C.J., Levings C.S. III,  
PD "Nucleotide sequence of the F1-ATPase alpha subunit from maize  
PE mitochondria.",  
PF Plant Physiol. 79:571-577(1985).  
PG [2]  
PH SEQUENCE FROM N.A.  
PI MEDLINE=88311189; PubMed=2900697;  
PJ Isaac B.C., Bernick A., Puchner C.M., Puchner C.T.

U

K1 "Complex organization of the soybean mitochondrial genome:

accionaria.";

## LET

Schulte E., Staubach S., Laser B., Kuec  
Wheat mitochondrial DNA: organization

Schulte E., Staubach S., Laser B., Kueck U.;  
Wheat mitochondrial DNA: organization and sequences of the atpA and rbcL genes."



```

RL Nucleic Acids Res. 17:7531-7531 (1989).
CC -!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC GRADIENT ACROSS THE MEMBRANE. THE ALPHA CHAIN IS A REGULATORY
CC SUBUNIT.
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
CC H(+) (Out).
CC -!- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC HAS THREE MAIN SUBUNITS: A, B AND C.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
CC -!- SIMILARITY: Belongs to the ATPase alpha/beta chains family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X15918; CAA34060.1; -.
CC PIR; S06007; PWTAM.
CC HSSP; P19483; 1BMF.
CC InterPro; IPR000793; ATPase_a/bc.
CC InterPro; IPR000194; ATPase_a/bcentre.
CC InterPro; IPR004100; ATPase_a/bn.
CC InterPro; IPR000790; ATPase_ac.
CC InterPro; IPR005294; ATPsynthF1_alpha.
CC Pfam; PF00006; ATP-synt_ab; 1.
CC Pfam; PF00306; ATP-synt_ab_C; 1.
CC Pfam; PF02874; ATP-synt_ab_N; 1.
CC ProDom; PD001099; ATPase_ac; 1.
CC TIGRFAMs; TIGR00962; atpA; 1.
CC PROSITE; PS00152; ATPASE ALPHA BETA; 1.
CC KW ATP synthase; CF(1); Hydrogen ion transport;
CC Hydrolase; ATP-binding; Mitochondrion.
CC NP_BIND 171 178 ATP (BY SIMILARITY).
CC FT ACT_SITE 373 373 BY SIMILARITY.
CC SQ SEQUENCE 509 AA; 55264 MW; 2BD7893B255EF66B CRC64;

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Query Match 40.2%; Score 51.5; DB 1; Length 509;
Best Local Similarity 42.3%; Pred. No. 8.4;
Matches 11; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

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QY 1 DVLKKTGTVV-LHAGKALGAVADTI 25
Db 88 DLVKTGTSIVDPVPGKALGRVVDAL 113

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Search completed: December 10, 2003, 20:28:06  
Job time : 12 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 10, 2003, 20:26:11 ; Search time 21 Seconds  
(without alignments)  
123.645 Million cell updates/sec

Title: US-09-936-895-3

Perfect score: 128

Sequence: 1 DVLKKTGTVALHAGKAALGAVADTISQ 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: PIR 76:\*

1: piri:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	128	100.0	27	2 A53727	dermasectin b - tw
2	128	100.0	78	2 B54897	dermasectin b i pr
3	110	85.9	34	2 A40298	dermasectin - Sauv
4	53.5	41.8	81	1 JN0462	adenoregulin precu
5	51.5	40.2	327	4 S29876	probable H+transp
6	51.5	40.2	506	2 S33922	H+-transporting tw
7	51.5	40.2	506	2 S45508	H+-transporting tw
8	51.5	40.2	507	2 JN0769	H+-transporting tw
9	51.5	40.2	507	2 A26760	H+-transporting tw
10	51.5	40.2	508	1 PWNAM	H+-transporting tw
11	51.5	40.2	508	2 S26979	H+-transporting tw
12	51.5	40.2	508	2 S29792	H+-transporting tw
13	51.5	40.2	509	1 PWTAM	H+-transporting tw
14	51.5	40.2	509	1 PWRZAM	H+-transporting tw
15	51.5	40.2	509	1 S19997	H+-transporting tw
16	51.5	40.2	510	2 S19261	H+-transporting tw
17	51	39.8	334	2 A72217	Holliday junction
18	50.5	39.5	507	1 PWRPA	H+-transporting tw
19	50.5	39.5	507	2 S12309	H+-transporting tw
20	50.5	39.5	590	2 A96691	hypothetical prote
21	50	38.1	417	2 A61454	H+-transporting tw
22	49.5	38.7	509	1 PWNAC	purine nucleoside
23	49	38.3	236	2 G90007	probable transcrip
24	49	38.3	256	2 F83103	H+-transporting tw
25	48.5	37.9	317	2 H70805	hypothetical prote
26	48.5	37.9	491	2 S17916	H+-transporting tw
27	48.5	37.9	511	2 S07316	H+-transporting tw
28	48	37.5	396	2 H97500	hypothetical prote
29	48	37.5	396	2 AD2719	conserved hypothet.

30 48 37.5 495 2 H82762  
31 48 37.5 694 2 E97630  
32 48 37.5 694 2 AH2853  
33 48 37.5 705 2 T18547  
34 48 37.5 718 2 A81122  
35 48 37.5 1294 2 T18546  
36 47.5 37.1 642 2 T06014  
37 47 36.7 29 2 A61613  
38 47 36.7 753 2 D81219  
39 47 36.7 753 2 F81991  
40 46.5 36.3 509 2 T11937  
41 46.5 36.3 557 2 C84146  
42 46 35.9 517 2 G75593  
43 45.5 35.5 513 2 S25955  
44 45.5 35.5 558 2 E97203  
45 45.5 35.5 1259 2 S25954

#### ALIGNMENTS

##### RESULT 1

A53727

dermasectin b - two-colored leaf frog

C/Species: Phyllomedusa bicolor (two-colored leaf frog)

C/Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 09-Apr-1998

C/Accession: A53727

R/Mor, A.; Amiche, M.; Nicolas, P.

Biochemistry 33, 6642-6650, 1994

A/Title: Structure, synthesis, and activity of dermasectin b, a novel vertebrate defens

A/Reference number: A53727; MUID:94263975; PMID:8204601

A/Accession: A53727

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-27 <MOR>

C/Suprafamily: dermasectin precursor; dermorphin precursor amino-terminal homology

C/Keywords: skin

Query Match 100.0%; Score 128; DB 2; Length 27;

Best Local Similarity 100.0%; Pred. No. 6.9e-12;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVLKKTGTVALHAGKAALGAVADTISQ 27

DB 1 DVLKKTGTVALHAGKAALGAVADTISQ 27

##### RESULT 2

B54897

dermasectin b I precursor - two-colored leaf frog

C/Species: Phyllomedusa bicolor (two-colored leaf frog)

C/Date: 23-Mar-1995 #sequence\_revision 23-Mar-1995 #text\_change 16-Jul-1999

C/Accession: B54897

R/Amiche, M.; Ducancel, F.; Mor, A.; Boulain, J.C.; Menez, A.; Nicolas, P.

J. Biol. Chem. 269, 17847-17852, 1994

A/Title: Precursors of vertebrate peptide antibiotics dermasectin b and adenoregulin ha

A/Reference number: A54897; MUID:94299491; PMID:8074751

A/Accession: B54897

A/Molecule type: mRNA

A/Residues: 1-78 <AMI>

A/Cross-references: GB:X72387; NID:9505483; PIDN:CAAS1080.1; PID:9505484

C/Suprafamily: dermasectin precursor; dermorphin precursor amino-terminal homology

C/Keywords: amidated carboxyl end; antibiotic; antifungal; skin

F1-44/Domain: dermorphin precursor amino-terminal homology <DER>

F1-22/Domain: signal sequence #status predicted <SIG>

F23-44/Domain: propeptide #status predicted <PRO>

F49-75/Product: dermasectin b I #status experimental <WAT>

F75/Modified site: amidated carboxyl end (Gln) (amide in mature form from following gl)

Query Match

Best Local Similarity 100.0%; Score 128; DB 2; Length 78;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

### RESULT 3

Query Match 85.9%; Score 110; DB 2; Length 34;

Query Match 40.2%; Score 51.5; DB 4; Length 327;  
Best Local Similarity 42.3%; Pred. No. 8.8;  
Matches 11; Conservative 7; Mismatches 7; Indels

Qy	1	DVLKIGTVA-LHAGKAALGAVADTI	25
	::: :	:     :	:
Db	88	DLVRTGSIVDPAGKAMLRVVDAL	113

## RESULT 4

RESULT 6

S33922

HH-transporting two-sector ATPase (EC 3.6.3.14) alpha chain - suga

Alternate names: Atpase alpha chain

C-Species: mitochondrion Beta vulgaris var. altissima (sugar beet)

C-Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 03

C-Accession: S33922

R-Senda, M.; Mikami, T.; Kinoshita, T.

Curr. Genet. 24, 164-170, 1993

A-Title: The sugar beet mitochondrial gene for the Atpase alpha-sub

A-Reference number: S33922; NUID:93365027; PMID:8358823

A-Accession: S33922

A>Status: not compared with conceptual translation

A-Molecule type: DNA

A-Residues: 1-506 <SEN>

A-Cross-references: GB:D15065; NID:G285631; PID:BAA03664.1; PID:G

A-Genetics:

A-Genes: atpA

A:Gene: atpA  
 A:Genome: mitochondrion  
 C:Superfamily: H<sup>+</sup>-transporting ATP synthase alpha chain; H<sup>+</sup>-transporting ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrial F<sub>1</sub>F<sub>0</sub>-ATP synthase  
 F:171-178/Region: nucleotide-binding motif A (P-loop)  
 F:205-377/Domain: H<sup>+</sup>-transporting ATP synthase alpha chain homology <ATP>

```

1  DVLKIGTVA-LHAGKAALGAVADTI 25
|::|:|::|::|::|::|::|:
88 DLVKRTGSIVDPAGKAMLGKRWVDAL 113

```

C:\Date: 15-Jul-1995 #sequence\_revision 23-Feb-1996 #text\_change 03-Jun-2002  
C:\Accession: S46508, S46507, S51586; S29535; S29536.

X., Collin, S.; Davies, D.R.; Thomas, C.M.  
Mol. Biol. 25, 91-103, 1994  
A/Title: Differential screening of mitochondrial cDNA libraries from male-fertile and cy  
A/Reference number: S46505; MUID:94272017; PMID:8003700  
A/Accession: S46508  
A/Molecule type: DNA  
A/Residues: 1-506 <XUE>  
A/Cross-references: EMBL:X68691  
A/Experimental source: male-sterile CMS  
A/Accession: S46507  
A/Molecule type: DNA  
A/Residues: 1-506 <XUE>  
A/Cross-references: EMBL:X68690  
A/Experimental source: male-fertile MF  
A/Note: The authors translated the codon GAT for residue 207 as Val  
R.Xue, Y.  
submitted to the EMBL Data Library, October 1992  
A/Reference number: S51586  
A/Accession: S51586  
A/Molecule type: DNA  
A/Residues: 1-447, 'L', 449, 'G', 451-453, 'D', 455-506 <XUE>  
A/Cross-references: EMBL:X68691; NID:G396759; PIDN:CAA48650.1; PID:G396760  
A/Experimental source: male-sterile CMS  
R.Xue, Y.; Davies, D.R.; Collin, S.; Thomas, C.M.  
submitted to the EMBL Data Library, October 1992  
A/Description: Molecular characterization of mitochondrial ATPase subunit A from cyto  
A/Reference number: S29535  
A/Accession: S29535  
A/Molecule type: DNA  
A/Residues: 1-447, 'L', 449, 'G', 451-453, 'D', 455-506 <XUE>  
A/Cross-references: EMBL:X68690; NID:G11262; PIDN:CAA48649.1; PID:G11263  
A/Experimental source: male-fertile MF  
C/Genetics:  
A/Gene: atpA  
A/Genome: mitochondrion  
C/Superfamily: H+-transporting ATP synthase alpha chain; H+-transporting ATP synthase al  
C/Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; nuc  
F:171-178/Region: nucleotide-binding motif A (P-loop)  
F:205-377/Domain: H+-transporting ATP synthase alpha chain homology <ATP>  
Query Match 40.2%; Score 51.5; DB 2; Length 506;  
Best Local Similarity 42.3%; Pred. No. 14;  
Matches 11; Conservative 7; Mismatches 7; Indels 1; Gaps 1;  
QY 1 DVLKKIGTVA-LHAGKALGAVADTI 25  
DB 88 DLVKRTGSIVDPAGKAMGLGRVVDAL 113  
RESULT 8  
JN0769  
H+-transporting two-sector ATPase (EC 3.6.3.14) alpha chain - garden pea mitochondrion  
N/Alternate names: ATP synthase; ATPase; F1F0-ATPase alpha chain  
C/Species: mitochondrion Pisum sativum (garden pea)  
C/Date: 30-Sep-1993 #sequence\_revision 20-Aug-1994 #text\_change 03-Jun-2002  
C/Accession: JN0769  
R.Morikami, A.; Nakamura, K.  
BioSci. Biotechnol. Biochem. 57, 1530-1535, 1993  
A/Title: Transcript map of oppositely oriented pea mitochondrial genes encoding the alph  
A/Reference number: JN0769; MUID:94033860; PMID:7764223  
A/Accession: JN0769  
A/Molecule type: DNA  
A/Residues: 1-507 <MOR>  
A/Cross-references: GB:D14698; NID:G286139; PIDN:BA003524.1; PID:G286140  
C/Comment: This enzyme is essential in the translocation of H+ through the inner mitoch  
C/Genetics:  
A/Genome: mitochondrion  
C/Superfamily: H+-transporting ATP synthase alpha chain; H+-transporting ATP synthase al  
C/Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; nuc  
F:171-178/Region: nucleotide-binding motif A (P-loop)  
F:205-377/Domain: H+-transporting ATP synthase alpha chain homology <ATP>

Query Match 40.2%; Score 51.5; DB 2; Length 507;  
Best Local Similarity 42.3%; Pred. No. 14;  
Matches 11; Conservative 7; Mismatches 7; Indels 1; Gaps 1;  
QY 1 DVLKKIGTVA-LHAGKALGAVADTI 25  
DB 88 DLVKRTGSIVDPAGKAMGLGRVVDAL 113  
RESULT 9  
A26760  
H+-transporting two-sector ATPase (EC 3.6.3.14) alpha chain - garden pea mitochondrion  
C/Species: mitochondrion Pisum sativum (garden pea)  
C/Date: 09-May-1988 #sequence\_revision 09-May-1988 #text\_change 03-Jun-2002  
C/Accession: A26760  
R.Morikami, A.; Nakamura, K.  
J. Biochem. 101, 967-976, 1987  
A/Title: Structure and expression of pea mitochondrial F1ATPase alpha-subunit gene and  
A/Reference number: A26760; MUID:87279992; PMID:2886497  
A/Accession: A26760  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: DNA  
A/Residues: 1-507 <MOR>  
C/Genetics:  
A/Genome: mitochondrion  
C/Superfamily: H+-transporting ATP synthase alpha chain; H+-transporting ATP synthase al  
C/Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; nuc  
F:171-178/Region: nucleotide-binding motif A (P-loop)  
F:205-377/Domain: H+-transporting ATP synthase alpha chain homology <ATP>  
Query Match 40.2%; Score 51.5; DB 2; Length 507;  
Best Local Similarity 42.3%; Pred. No. 14;  
Matches 11; Conservative 7; Mismatches 7; Indels 1; Gaps 1;  
QY 1 DVLKKIGTVA-LHAGKALGAVADTI 25  
DB 88 DLVKRTGSIVDPAGKAMGLGRVVDAL 113  
RESULT 10  
PZMZAM  
H+-transporting two-sector ATPase (EC 3.6.3.14) alpha chain - maize mitochondrion  
N/Alternate names: ATPase alpha chain  
C/Species: mitochondrion Zea mays (maize)  
C/Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 14-Dec-2001  
C/Accession: A23757  
R.Braun, C.J.; Levings III, C.S.  
Plant Physiol. 79, 571-577, 1985  
A/Title: Nucleotide sequence of the F1-ATPase alpha subunit gene from maize mitochondri  
A/Reference number: A23757  
A/Accession: A23757  
A/Molecule type: DNA  
A/Residues: 1-508 <BRA>  
A/Cross-references: EMBL:M16222; NID:G342633; PIDN:AAA70269.1; PID:G897619  
C/Genetics:  
A/Gene: atpA  
A/Genome: mitochondrion  
C/Superfamily: H+-transporting ATP synthase alpha chain; H+-transporting ATP synthase al  
C/Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; nuc  
F:171-178/Region: nucleotide-binding motif A (P-loop)  
F:205-377/Domain: H+-transporting ATP synthase alpha chain homology <ATP>  
F:268-273/Region: nucleotide-binding motif B  
F:177/Binding site: ATP (lys) #status predicted  
F:376/Active site: Arg #status predicted  
Query Match 40.2%; Score 51.5; DB 1; Length 508;  
Best Local Similarity 42.3%; Pred. No. 14;  
Matches 11; Conservative 7; Mismatches 7; Indels 1; Gaps 1;  
QY 1 DVLKKIGTVA-LHAGKALGAVADTI 25  
DB 88 DLVKRTGSIVDPAGKAMGLGRVVDAL 113

RESULT 11  
 S26979  
 H+-transporting two-sector ATPase (EC 3.6.3.14) alpha chain - kidney bean mitochondrion  
 N/Alternate names: ATPase alpha chain  
 C/Species: mitochondrion Phaseolus vulgaris (kidney bean)  
 C/Date: 23-Apr-1993 #sequence\_revision 23-Apr-1993 #text\_change 03-Jun-2002  
 C/Accession: S26979  
 R/Chase, C.D.; Ortega, V.M.  
 Curr. Genet. 22, 147-153, 1992  
 A/Title: Organization of ATPa coding and 3' flanking sequences associated with cytoplasm  
 A/Reference number: S26979; MUID:93046798; PMID:14231717  
 A/Accession: S26979  
 A/Molecule type: DNA  
 A/Residues: 1-508 <CHA>  
 A/Cross-references: EMBL:M64246; NID:g169317; PIDN:AA801582.1; PID:g169318  
 A/Note: the authors translated the codon GGG for residue 257 as Cys  
 C/Genetics:  
 A/Gene: atpa  
 A/Genome: mitochondrion  
 C/Superfamily: H+-transporting ATP synthase alpha chain; H+-transporting ATP synthase al  
 C/Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; nuc  
 F/171-178/Region: nucleotide-binding motif A (P-loop)  
 F/205-377/Domain: H+-transporting ATP synthase alpha chain homology <ATP>  
 Query Match 40.2%; Score 51.5; DB 2; Length 508;  
 Best Local Similarity 42.3%; Pred. No. 14;  
 Matches 11; Conservative 7; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 DVLKKGITVA-LHAGKAALGAVADTI 25  
 DB 88 DLVKRTGSIVDPAGKAMLGRRVVDAL 113  
 RESULT 12  
 S29792  
 H+-transporting two-sector ATPase (EC 3.6.3.14) alpha chain - soybean mitochondrion  
 N/Alternate names: ATPase alpha chain  
 C/Species: mitochondrion Glycine max (soybean)  
 C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 03-Jun-2002  
 C/Accession: S29792; S29873  
 R/Chanut, P.A.; Grabau, E.A.; Gesteland, R.P.  
 Curr. Genet. 23, 234-247, 1993  
 A/Title: Complex organization of the soybean mitochondrial genome: recombination repeats  
 A/Reference number: S29792; MUID:93169687; PMID:8435853  
 A/Accession: S29792  
 A/Molecule type: DNA  
 A/Residues: 1-508 <CHA>  
 A/Cross-references: EMBL:Z14031; NID:g22738; PIDN:CA78407.1; PID:g22739  
 C/Genetics:  
 A/Gene: atpa  
 A/Genome: mitochondrion  
 C/Superfamily: H+-transporting ATP synthase alpha chain; H+-transporting ATP synthase al  
 C/Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; nuc  
 F/171-178/Region: nucleotide-binding motif A (P-loop)  
 F/205-377/Domain: H+-transporting ATP synthase alpha chain homology <ATP>  
 Query Match 40.2%; Score 51.5; DB 2; Length 508;  
 Best Local Similarity 42.3%; Pred. No. 14;  
 Matches 11; Conservative 7; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 DVLKKGITVA-LHAGKAALGAVADTI 25  
 DB 88 DLVKRTGSIVDPAGKAMLGRRVVDAL 113  
 RESULT 13  
 PWTAM  
 H+-transporting two-sector ATPase (EC 3.6.3.14) alpha chain - wheat mitochondrion  
 C/Species: mitochondrion Triticum aestivum (common wheat)  
 C/Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 14-Dec-2001  
 C/Accession: S06007  
 R/Schulte, E.; Staubach, S.; Laser, B.; Kueck, U.

Nucleic Acids Res. 17, 7531, 1989  
 A/Title: Wheat mitochondrial DNA: organization and sequences of the atpa and atp9 ge  
 A/Reference number: S06007; MUID:90016824; PMID:2529479  
 A/Accession: S06007  
 A/Status: translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-509 <SCH>  
 A/Cross-references: EMBL:X15918  
 C/Genetics:  
 A/Gene: atpa  
 A/Genome: mitochondrion  
 C/Superfamily: H+-transporting ATP synthase alpha chain; H+-transporting ATP synthas  
 C/Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion;  
 F/171-178/Region: nucleotide-binding motif A (P-loop)  
 F/205-377/Domain: H+-transporting ATP synthase alpha chain homology <ATP>  
 F/268-273/Region: nucleotide-binding motif B  
 F/177/Binding site: ATP (Lys) #status predicted  
 F/376/Active site: Arg #status predicted  
 Query Match 40.2%; Score 51.5; DB 1; Length 509;  
 Best Local Similarity 42.3%; Pred. No. 14;  
 Matches 11; Conservative 7; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 DVLKKGITVA-LHAGKAALGAVADTI 25  
 DB 88 DLVKRTGSIVDPAGKAMLGRRVVDAL 113  
 RESULT 14  
 PWRZAM  
 H+-transporting two-sector ATPase (EC 3.6.3.14) alpha chain - rice mitochondrion  
 C/Species: mitochondrion Oryza sativa (rice)  
 C/Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 14-Dec-2001  
 C/Accession: JQ0411  
 R/Kadowaki, K.; Kazama, S.; Suzuki, T.  
 Nucleic Acids Res. 18, 1302, 1990  
 A/Title: Nucleotide sequence of the F1-ATPase alpha subunit gene from rice mitochond  
 A/Reference number: JQ0411; MUID:90206808; PMID:2138730  
 A/Accession: JQ0411  
 A/Molecule type: DNA  
 A/Residues: 1-509 <KAD>  
 A/Cross-references: EMBL:X51422; NID:g13958; PIDN:CAA35787.1; PID:g13959  
 C/Genetics:  
 A/Gene: atpa  
 A/Genome: mitochondrion  
 C/Superfamily: H+-transporting ATP synthase alpha chain; H+-transporting ATP synthas  
 C/Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion;  
 F/171-178/Region: nucleotide-binding motif A (P-loop)  
 F/205-377/Domain: H+-transporting ATP synthase alpha chain homology <ATP>  
 F/268-273/Region: nucleotide-binding motif B  
 F/177/Binding site: ATP (Lys) #status predicted  
 F/376/Active site: Arg #status predicted  
 Query Match 40.2%; Score 51.5; DB 1; Length 509;  
 Best Local Similarity 42.3%; Pred. No. 14;  
 Matches 11; Conservative 7; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 DVLKKGITVA-LHAGKAALGAVADTI 25  
 DB 88 DLVKRTGSIVDPAGKAMLGRRVVDAL 113  
 RESULT 15  
 S10997  
 H+-transporting two-sector ATPase (EC 3.6.3.14) alpha chain - common sunflower mitoch  
 C/Species: mitochondrion Helianthus annuus (common sunflower)  
 C/Date: 18-Feb-1994 #sequence\_revision 03-Aug-1995 #text\_change 03-Jun-2002  
 C/Accession: S10997; S10974; S17799; S52010; S48854  
 R/Koehler, R.H.; Loesel, A.; Zetsche, K.  
 Nucleic Acids Res. 18, 4588, 1990  
 A/Title: Nucleotide sequence of the F1-ATPase alpha subunit gene of sunflower mitoch  
 A/Reference number: S10997; MUID:90356396; PMID:2143817  
 A/Accession: S10997

Molecule type: DNA  
 A/Residues: 1-510 <KOE>  
 A/Cross-references: EMBL:X53537; NID:g12577; PIDN:CAA37613.1; PID:g758362  
 A/Experimental source: line Baso  
 R/Siculella, L.; D'Amrosio, L.; de Tuglie, A.D.; Gallerani, R.  
 Nucleic Acids Res. 18, 4599, 1990  
 A/Title: Minor differences in the primary structures of atpa genes coded on the mtDNA of  
 A/Reference number: S10374; MUID:90356407; PMID:2143818  
 A/Accession: S10974  
 A/Molecule type: DNA  
 A/Residues: 1-510 <SIC>  
 A/Cross-references: EMBL:X52838; NID:g12988; PIDN:CAA37022.1; PID:g12989  
 A/Experimental source: strain HA89  
 R/Koehler, R.H.; Horn, R.; Loessl, A.; Zetsche, K.  
 Mol. Gen. Genet. 227, 369-376, 1991  
 A/Title: Cytoplasmic male sterility in sunflower is correlated with the co-transcription  
 A/Reference number: S16528; MUID:91326025; PMID:1714033  
 A/Accession: S17799  
 A/Status: translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-510 <KOA>  
 A/Cross-references: EMBL:X55963; NID:g12985; PIDN:CAA39428.1; PID:g12986  
 A/Experimental source: line CMSBaso  
 R/Spasova, M.; Monner, P.; Leaver, C.J.; Petrov, P.; Atanassov, A.; Nijkamp, H.J.J.; H  
 plant Mol. Biol. 26, 1819-1831, 1994  
 A/Title: Characterisation and expression of the mitochondrial genome of a new type of cy  
 A/Reference number: S52010; MUID:95161706; PMID:7858220  
 A/Accession: S52010  
 A/Status: translation not shown  
 A/Molecule type: DNA  
 A/Residues: 293-510 <SPA>  
 A/Cross-references: EMBL:X82386; NID:g563544; PIDN:CAA57786.1; PID:g563545  
 C/Genetics:  
 A/Gene: atpa  
 A/Genome: mitochondrion  
 C/Superfamily: H<sup>+</sup>-transporting ATP synthase alpha chain; H<sup>+</sup>-transporting ATP synthase al  
 C/Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; nuc  
 P/171-178/Region: nucleotide-binding motif A (P-loop)  
 F/205-377/Domain: H<sup>+</sup>-transporting ATP synthase alpha chain homology <ATP>

Query Match 40.2%; Score 51.5; DB 2; Length 510;  
 Best Local Similarity 42.3%; Pred. No. 14;  
 Matches 11; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

QY 1 DVLKKIGTVA-LHAGKAALGAVADTI 25  
 Db 88 DLVKTGSIQVDPAGKAMLGRRVVDAL 113

Search completed: December 10, 2003, 20:29:27  
 Job time : 22 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 10, 2003, 20:27:46 ; Search time 30 Seconds  
(without alignments)  
167.385 Million cell updates/sec

Title: US-09-936-885-3

Perfect score: 128

Sequence: 1 DVLKXIGTVALHAGKAALGAVADTISQ 27

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
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7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
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10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	128	100.0	31	14	US-10-038-045-13
2	110	85.9	33	9	US-09-917-340-21
3	110	85.9	33	11	US-09-908-139-23
4	110	85.9	33	15	US-10-197-954-45
5	110	85.9	34	14	US-10-038-045-7
6	105	82.0	34	9	US-09-917-340-22
7	105	82.0	34	14	US-10-038-045-8
8	99.5	77.7	32	9	US-09-030-619-201
9	73	57.0	19	14	US-10-038-045-16
10	59	46.1	30	11	US-09-908-139-20
11	55	43.0	18	14	US-10-038-045-11
12	54	42.2	29	11	US-09-908-139-19
13	54	42.2	29	11	US-09-908-139-21
14	51.5	40.2	33	14	US-10-038-045-14
15	49	38.3	287	9	US-09-864-761-42836

16 48.5 37.9 30 9 US-09-917-340-23 Sequence 23, Appl  
17 48.5 37.9 30 14 US-10-038-045-9 Sequence 9, Appl  
18 48 37.5 171 10 US-09-764-864-1225 Sequence 1225, Ap  
19 48 37.5 1258 10 US-09-867-852-107 Sequence 107, App  
20 48 37.5 1295 10 US-09-738-626-6480 Sequence 6480, Ap  
21 47.5 37.1 154 15 US-10-156-761-14882 Sequence 14882, A  
22 47.5 37.1 590 10 US-09-893-817-2 Sequence 2, Appl  
23 47.5 37.1 642 10 US-09-893-817-24 Sequence 24, Appl  
24 47 36.7 29 9 US-09-917-340-30 Sequence 30, Appl  
25 47 36.7 288 10 US-09-738-626-4286 Sequence 4286, Ap  
26 46 35.9 445 10 US-09-738-626-3627 Sequence 3627, Ap  
27 46 35.9 557 15 US-10-156-761-9608 Sequence 9608, Ap  
28 46 35.9 1276 15 US-10-156-761-10509 Sequence 10509, A  
29 45 35.2 26 11 US-09-908-139-17 Sequence 17, Appl  
30 45 35.2 97 9 US-09-887-586A-40 Sequence 40, Appl  
31 45 35.2 97 9 US-09-903-012-40 Sequence 40, Appl  
32 45 35.2 97 11 US-09-900-797-40 Sequence 40, Appl  
33 45 35.2 4961 12 US-10-114-153-64 Sequence 64, Appl  
34 44 34.4 29 9 US-09-917-340-31 Sequence 31, Appl  
35 44 34.4 29 11 US-09-908-139-24 Sequence 24, Appl  
36 44 34.4 2080 11 US-09-382-860-2 Sequence 2, Appl  
37 43 33.6 240 15 US-10-156-761-14602 Sequence 14602, A  
38 43 33.6 385 10 US-09-738-626-3888 Sequence 3888, Ap  
39 42.5 33.2 378 10 US-09-731-872-406 Sequence 406, App  
40 42.5 33.2 378 12 US-09-876-997-406 Sequence 406, App  
41 42.5 33.2 910 15 US-10-156-761-11103 Sequence 11103, A  
42 42.5 33.2 911 10 US-09-853-754-4 Sequence 4, Appl  
43 42.5 33.2 911 12 US-10-302-896-4 Sequence 4, Appl  
44 42.5 33.2 911 15 US-10-227-353-4 Sequence 4, Appl  
45 42.5 33.2 922 10 US-09-855-754-6 Sequence 6, Appl

#### ALIGNMENTS

#### RESULT 1

US-10-038-045-13  
; Sequence 13, Application US/10038045  
; Publication No. US20020150964A1  
; GENERAL INFORMATION:

APPLICANT: Mor, Amram

Vouldoukis, Ioannis  
Nicolas, Pierre

TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESS: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/038,045

FILING DATE: 02-Jan-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/181,941

FILING DATE: 28-Oct-1998

APPLICATION NUMBER: US 08/574,701

FILING DATE: 19-DEC-1995

APPLICATION NUMBER: FR 95 07831

FILING DATE: 29-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 3909-0021-999

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE

## INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:  
LENGTH: 31 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. US20020150964A1e  
SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-10-038-045-13

Query Match 100.0%; Score 128; DB 14; Length 31;  
Best Local Similarity 100.0%; Pred. No. 4.6e-13;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVLKKGITVALHAGKAALGAVADTISQ 27  
DB 5 DVLKKGITVALHAGKAALGAVADTISQ 31

## RESULT 2

US-09-917-340-21  
Sequence 21, Application US/09917340  
Patent No. US20020090369A1

## GENERAL INFORMATION:

APPLICANT: Murphy, Christopher J.  
APPLICANT: McAnulty, Jonathan F.  
APPLICANT: Reid, Ted W.  
TITLE OF INVENTION: Transplant Media  
FILE REFERENCE: TPLANT-06468  
CURRENT APPLICATION NUMBER: US/09/917,340  
CURRENT FILING DATE: 2001-07-29  
PRIOR APPLICATION NUMBER: 60/221,632  
PRIOR FILING DATE: 2000-07-28  
PRIOR APPLICATION NUMBER: 60/249,602  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/290,932  
PRIOR FILING DATE: 2001-05-15  
NUMBER OF SEQ ID NOS: 96  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 21  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Phyllomedusa sauvagae  
US-09-917-340-21

Query Match 85.9%; Score 110; DB 9; Length 33;  
Best Local Similarity 84.6%; Pred. No. 3.2e-10;  
Matches 22; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VLKKGITVALHAGKAALGAVADTISQ 27  
DB 6 MLKKGITVALHAGKAALGAAADTISQ 31

## RESULT 3

US-09-908-139-23

Sequence 23, Application US/09908139  
Publication No. US2003009694A1

## GENERAL INFORMATION:

APPLICANT: Hancock, Robert E. W.  
APPLICANT: Gough, Monisha A.  
APPLICANT: Patrzykat, Aleksander  
APPLICANT: Woods, Donald  
APPLICANT: Jia, Xiaoyan  
TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC  
PEPTIDES AND METHODS OF USE THEREFOR  
FILE REFERENCE: 07422/016001  
CURRENT APPLICATION NUMBER: US/09/908,139  
CURRENT FILING DATE: 2001-07-17

PRIOR APPLICATION NUMBER: 09/143,124  
PRIOR FILING DATE: 1998-08-28  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 23  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: antimicrobial cationic peptide  
US-09-908-139-23

Query Match 85.9%; Score 110; DB 11; Length 33;  
Best Local Similarity 84.6%; Pred. No. 3.2e-10;  
Matches 22; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VLKKGITVALHAGKAALGAVADTISQ 27  
DB 6 MLKKGITVALHAGKAALGAAADTISQ 31

## RESULT 4

US-10-197-954-45

Sequence 45, Application US/10197954  
Publication No. US20030119021A1

## GENERAL INFORMATION:

APPLICANT: K'ater, Hubert  
APPLICANT: Siddiqi, Suhail  
APPLICANT: Little, Daniel  
TITLE OF INVENTION: Capture Compounds, Collections Thereof  
TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex  
TITLE OF INVENTION: Compositions  
FILE REFERENCE: 24743-2305  
CURRENT APPLICATION NUMBER: US/10/197,954  
CURRENT FILING DATE: 2002-07-16  
PRIOR APPLICATION NUMBER: 60/306,019  
PRIOR FILING DATE: 2001-07-16  
PRIOR APPLICATION NUMBER: 60/314,123  
PRIOR FILING DATE: 2001-08-21  
PRIOR APPLICATION NUMBER: 60/363,433  
PRIOR FILING DATE: 2002-03-11  
NUMBER OF SEQ ID NOS: 149  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 45  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-197-954-45

Query Match 85.9%; Score 110; DB 15; Length 33;  
Best Local Similarity 84.6%; Pred. No. 3.2e-10;  
Matches 22; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VLKKGITVALHAGKAALGAVADTISQ 27  
DB 6 MLKKGITVALHAGKAALGAAADTISQ 31

## RESULT 5

US-10-038-045-7

Sequence 7, Application US/10038045  
Publication No. US20020150964A1

## GENERAL INFORMATION:

APPLICANT: Mor, Anram  
APPLICANT: Vouldoukis, Ioannis  
APPLICANT: Nicolas, Pierre  
TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION  
OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York



```

Best Local Similarity 80.8%; Pred. No. 2e-09;
Matches 21; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 VLKIGTVALHAGKAALGAVADTISQ 27
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Db 6 MLKKIGTMALHAGKAALGAAANTISQ 31

RESULT 7
US-10-038-045-8
; Sequence 8, Application US/10038045
; Publication No. US20020150964A1
; GENERAL INFORMATION:
; APPLICANT: Mor, Amram
; Vouldoukis, Ioannis
; Nicolas, Pierre
; TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION
; OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/038,045
; FILING DATE: 02-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

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APPLICATION NUMBER: US 09/181,941  
FILING DATE: 28-Oct-1998  
APPLICATION NUMBER: US 08/574,701  
FILING DATE: 19-DEC-1995

APPLICATION NUMBER: PR 95 07831  
FILING DATE: 29-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A

```

REFERENCE/DOCKET NUMBER: 3909-0021-999
TELECOMMUNICATION INFORMATION:
    TELEPHONE: 650-493-4935
    TELEFAX: 650-493-5556
    TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 34 amino acids
        TYPE: amino acid
        STRANDEDNESS: single
        TOPOLOGY: linear
MOLECULE TYPE: NO. US20020150964Aile
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-038-045-8

Query Match      82.0%; Score 105; DB 14; Length 34;
Best Local Similarity 80.8%; Pred. No. 2e-09;
Matches 21; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      2 VLKKGITVALHAGKAALGAVADTTISQ 27
         :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB      6 MLKKIGTVALHAGKAALGAANTISQ 31

RESULT 8
US-09-030-619-201

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; Sequence 201, Application US/09030619B  
; Patent No. US20020035061A1

```

; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfile, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H. P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 660081.406
; CURRENT APPLICATION NUMBER: US/09/030.619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 201
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Phyllomedusa sauvagii
US-09-030-619-201

Query Match 77.7%; Score 99.5; DB 9; Length 32;
Best Local Similarity 84.6%; Pred. NO. 1.4e-08;
Matches 22; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 2 VLKKGITVALHAGKAALGAVADTISQ 27
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DB 6 MLKKLGTMLHAGKAALGA-ADTISQ 30

RESULT 9
US-10-038-045-16
; Sequence 16, Application US/10038045
; Publication No. US20020150964A1
; GENERAL INFORMATION:
; APPLICANT: Mor, Amram
; APPLICANT: Vouldoukis, Ioannis
; APPLICANT: Nicolas, Pierre
; TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION
; OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/038.045
; FILING DATE: 02-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; APPLICATION DATE:
; FILING DATE: 28-Oct-1998
; APPLICATION NUMBER: US 08/574,701
; FILING DATE: 19-DEC-1995
; APPLICATION NUMBER: FR 95 07831
; FILING DATE: 29-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Cortuzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 3909-0021-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 16:

```

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-038-045-16

Query Match 57.0%; Score 73; DB 14; Length 19;
Best Local Similarity 93.8%; Pred. NO. 0.00011;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 HAGKAALGAVADTISQ 27
:||||:||||:||||:
DB 1 HAGKAALGAAADTISQ 16

RESULT 10
US-09-908-139-20
; Sequence 20, Application US/09908139
; Publication No. US20030096949A1
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Gough, Monisha A.
; APPLICANT: Patrzykat, Aleksander
; APPLICANT: Woods, Donald
; APPLICANT: Jia, Xiaoyan
; TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC
; TITLE OF INVENTION: PEPTIDES AND METHODS OF USE THEREFOR
; FILE REFERENCE: 07422/016001
; CURRENT APPLICATION NUMBER: US/09/908.139
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/143,124
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antimicrobial cationic peptide
US-09-908-139-20

Query Match 46.1%; Score 59; DB 11; Length 30;
Best Local Similarity 61.9%; Pred. NO. 0.028;
Matches 13; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 VLKKGITVALHAGKAALGAVA 22
:||||:||||:||||:
DB 6 MLKKAHVGKHVKGKALGAA 26

RESULT 11
US-10-038-045-11
; Sequence 11, Application US/10038045
; Publication No. US20020150964A1
; GENERAL INFORMATION:
; APPLICANT: Mor, Amram
; APPLICANT: Vouldoukis, Ioannis
; APPLICANT: Nicolas, Pierre
; TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION
; OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

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COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
FILING DATE: 02-Jan-2002  
APPLICATION NUMBER: US/10/038,045  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
FILING DATE: 28-Oct-1998  
APPLICATION NUMBER: US 08/574,701  
FILING DATE: 19-DEC-1995  
APPLICATION NUMBER: FR 95 07831  
FILING DATE: 29-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 3909-0021-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. US20020150964A1e  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-10-038-045-11

Query Match 43.0%; Score 55; DB 14; Length 18;  
Best Local Similarity 76.9%; Pred. No. 0.065;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 VLKIGTVALHAG 14  
DB 6 MLKLGTVLHAG 18

RESULT 12  
US-09-908-139-19  
; Sequence 19, Application US/09908139  
; Publication No. US20030096949A1  
; GENERAL INFORMATION:  
; APPLICANT: Hancock, Robert E. W.  
; APPLICANT: Gough, Monisha A.  
; APPLICANT: Patrzykat, Aleksander  
; APPLICANT: Woods, Donald  
; APPLICANT: Jia, Xiaoyan  
; TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC  
; FILE REFERENCE: 07422/016001  
; CURRENT APPLICATION NUMBER: US/09/908,139  
; CURRENT FILING DATE: 2001-07-17  
; PRIOR APPLICATION NUMBER: 09/143,124  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 29  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antimicrobial cationic peptide  
US-09-908-139-19

Query Match 42.2%; Score 54; DB 11; Length 29;  
Best Local Similarity 63.2%; Pred. No. 0.16;  
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 KKIQTVALHAGKALGAVA 22  
DB 6 MLKLGTVLHAG 18

RESULT 13  
US-09-908-139-21  
; Sequence 21, Application US/09908139  
; Publication No. US20030096949A1  
; GENERAL INFORMATION:  
; APPLICANT: Hancock, Robert E. W.  
; APPLICANT: Gough, Monisha A.  
; APPLICANT: Patrzykat, Aleksander  
; APPLICANT: Woods, Donald  
; APPLICANT: Jia, Xiaoyan  
; TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC  
; FILE REFERENCE: 07422/016001  
; CURRENT APPLICATION NUMBER: US/09/908,139  
; CURRENT FILING DATE: 2001-07-17  
; PRIOR APPLICATION NUMBER: 09/143,124  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21  
; LENGTH: 29  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antimicrobial cationic peptide  
US-09-908-139-21

Query Match 42.2%; Score 54; DB 11; Length 29;  
Best Local Similarity 63.2%; Pred. No. 0.16;  
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 KKIQTVALHAGKALGAVA 22  
DB 7 KKAHVGVKGVKALGAAA 25

RESULT 14  
US-10-038-045-14  
; Sequence 14, Application US/10038045  
; Publication No. US20020150964A1  
; GENERAL INFORMATION:  
; APPLICANT: Mor, Antram  
; APPLICANT: Voulgoukis, Ioannis  
; APPLICANT: Nicolas, Pierre  
; TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION  
; OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/038,045  
; FILING DATE: 02-Jan-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/181,941  
; FILING DATE: 28-Oct-1998  
; APPLICATION NUMBER: US 08/574,701  
; FILING DATE: 19-DEC-1995  
; APPLICATION NUMBER: FR 95 07831

DB 7 KKAHVGVKGVKALGAAA 25

RESULT 13  
US-09-908-139-21  
; Sequence 21, Application US/09908139  
; Publication No. US20030096949A1  
; GENERAL INFORMATION:  
; APPLICANT: Hancock, Robert E. W.  
; APPLICANT: Gough, Monisha A.  
; APPLICANT: Patrzykat, Aleksander  
; APPLICANT: Woods, Donald  
; APPLICANT: Jia, Xiaoyan  
; TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC  
; FILE REFERENCE: 07422/016001  
; CURRENT APPLICATION NUMBER: US/09/908,139  
; CURRENT FILING DATE: 2001-07-17  
; PRIOR APPLICATION NUMBER: 09/143,124  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21  
; LENGTH: 29  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antimicrobial cationic peptide  
US-09-908-139-21

QY 4 KKIQTVALHAGKALGAVA 22  
DB 7 KKAHVGVKGVKALGAAA 25

RESULT 14  
US-10-038-045-14  
; Sequence 14, Application US/10038045  
; Publication No. US20020150964A1  
; GENERAL INFORMATION:  
; APPLICANT: Mor, Antram  
; APPLICANT: Voulgoukis, Ioannis  
; APPLICANT: Nicolas, Pierre  
; TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION  
; OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/038,045  
; FILING DATE: 02-Jan-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/181,941  
; FILING DATE: 28-Oct-1998  
; APPLICATION NUMBER: US 08/574,701  
; FILING DATE: 19-DEC-1995  
; APPLICATION NUMBER: FR 95 07831

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RESULT 15
US/09-864-761-42836
US Sequence 42836, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED
FILE OF INVENTION: GENE EXPRESSION ANAL
FILE REFERENCE: AescmIca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/006656
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006657
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006654
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006659
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006652
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006658
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006653
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006652
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006651
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687

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OM protein - protein search, using sw model

Run on: December 10, 2003, 20:26:51 / Search time 21 Seconds  
(without alignments)  
54.400 Million cell updates/sec

Title: US-09-936-885-3

Perfect score: 128

Sequence: 1 DVLKXIGTVALHAGKAALGAVADTISQ 27

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:

- 1: /cgn2.6/ptodata/1/iaa/5A COMB.pdp.\*
- 2: /cgn2.6/ptodata/1/iaa/5B COMB.pdp.\*
- 3: /cgn2.6/ptodata/1/iaa/6A COMB.pdp.\*
- 4: /cgn2.6/ptodata/1/iaa/6B COMB.pdp.\*
- 5: /cgn2.6/ptodata/1/iaa/6C COMB.pdp.\*
- 6: /cgn2.6/ptodata/1/iaa/6D COMB.pdp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	128	100.0	31	4	US-09-181-941-13
2	110	85.9	33	3	US-09-143-124-23
3	110	85.9	34	4	US-09-181-941-7
4	105	82.0	34	4	US-09-181-941-8
5	99.5	77.7	32	4	US-09-030-619-201
6	73	57.0	19	4	US-09-181-941-16
7	59	46.1	30	3	US-09-143-124-20
8	55	43.0	18	4	US-09-181-941-11
9	54	42.2	29	3	US-09-143-124-19
10	54	42.2	29	3	US-09-143-124-21
11	51.5	40.2	33	4	US-09-181-941-14
12	49	38.3	265	4	US-09-252-991A-24310
13	48.5	37.9	30	4	US-09-181-941-9
14	48	37.5	1209	5	PCR-US95-04589-107
15	48	37.5	1258	2	US-08-310-912A-107
16	48	37.5	1258	3	US-09-301-085-107
17	48	37.5	1294	3	US-08-930-996A-10
18	45.5	35.5	625	4	US-09-252-991A-23005
19	45	35.2	26	3	US-09-143-124-17
20	45	35.2	97	4	US-09-398-395A-40
21	45	35.2	97	4	US-09-887-586A-40
22	45	35.2	97	4	US-09-895-752-40
23	45	35.2	97	4	US-09-903-012B-40
24	45	35.2	926	4	US-09-252-991A-31053
25	44	34.4	1039	4	US-09-143-124-24
26	44	34.4	1039	4	US-09-252-991A-28966
27	43.5	34.0	566	4	US-09-252-991A-24498

28	43.5	34.0	858	4	US-09-252-991A-17399	Sequence 17399, A
29	43	33.6	292	4	US-09-107-532A-5310	Sequence 5310, Ap
30	43	33.6	404	4	US-09-328-352-6747	Sequence 6747, Ap
31	43	33.6	1584	3	US-09-251-645-6	Sequence 6, Appl
32	42.5	33.2	469	4	US-09-252-991A-29009	Sequence 29009, A
33	42.5	33.2	911	3	US-08-460-269C-4	Sequence 4, Appl
34	42.5	33.2	922	3	US-08-460-269C-6	Sequence 6, Appl
35	42	32.8	27	4	US-09-030-619-170	Sequence 5, Appl
36	42	32.8	80	2	US-08-849-373-5	Sequence 5, Appl
37	42	32.8	116	4	US-09-199-637A-409	Sequence 409, Appl
38	42	32.8	359	4	US-09-252-991A-23051	Sequence 23051, A
39	42	32.8	383	4	US-09-252-991A-18049	Sequence 18049, A
40	42	32.8	400	4	US-08-311-731A-81	Sequence 81, Appl
41	42	32.8	409	4	US-08-311-731A-188	Sequence 188, Appl
42	42	32.8	458	4	US-09-252-991A-28585	Sequence 28585, A
43	42	32.8	501	4	US-09-328-352-5227	Sequence 5227, Ap
44	42	32.8	536	4	US-09-252-991A-33121	Sequence 33121, A
45	42	32.8	685	4	US-09-252-991A-31711	Sequence 31711, A

#### ALIGNMENTS

#### RESULT 1

US-09-181-941-13

/ Sequence 13, Application US/09181941

/ Patent No. 6440690

/ GENERAL INFORMATION:

/ APPLICANT: Mor, Amram

/ Vouldoukis, Ioannis

/ Nicolas, Pierre

/ TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION

/ OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS

/ NUMBER OF SEQUENCES: 16

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Pennie & Edmonds LLP

/ CITY: New York

/ STATE: NY

/ COUNTRY: USA

/ ZIP: 10036-2811

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Diskette

/ OPERATING SYSTEM: Windows

/ SOFTWARE: FastSeq for Windows Version 2.0b

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/09/181,941

/ FILING DATE: 28-Oct-1998

/ CLASSIFICATION: <Unknown>

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 08/574,701

/ FILING DATE: 19-DEC-1995

/ APPLICATION NUMBER: FR 95 07831

/ FILING DATE: 29-JUN-1995

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Coruzzi, Laura A

/ REGISTRATION NUMBER: 30,742

/ REFERENCE/DOCKET NUMBER: 3909-0021-999

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: 650-493-4935

/ TELEFAX: 650-493-5556

/ TELEX: 66141 PENNIE

/ INFORMATION FOR SEQ ID NO: 13:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 31 amino acids

/ TYPE: amino acid

/ STRANDEDNESS: single

/ TOPOLOGY: linear

/ MOLECULE TYPE: No. 6440690e

/ SEQUENCE DESCRIPTION: SEQ ID NO: 13:

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Query Match 100.0%; Score 128; DB 4; Length 31;  
Best Local Similarity 100.0%; Pred. No. 6.9e-14;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVLKKIGTVALHAGKAAALGAVADTISQ 27  
DB 5 DVLKKIGTVALHAGKAAALGAVADTISQ 31

RESULT 2  
US-09-143-124-23  
; Sequence 23, Application US/09143124  
; Patent No. 6288212  
; GENERAL INFORMATION:  
; APPLICANT: Hancock, Robert E. W.  
; APPLICANT: Gough, Monisha A.  
; APPLICANT: Patrzykat, Aleksander  
; APPLICANT: Woods, Donald  
; APPLICANT: Jia, Xiaoyan  
; TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC  
; TITLE OF INVENTION: PEPTIDES AND METHODS OF USE THEREFOR  
; FILE REFERENCE: 07422/016001  
; CURRENT APPLICATION NUMBER: US/09/143,124  
; CURRENT FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antimicrobial cationic peptide  
US-09-143-124-23

Query Match 85.9%; Score 110; DB 3; Length 33;  
Best Local Similarity 84.6%; Pred. No. 5.7e-11;  
Matches 22; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VLKKGITVALHAGKAAALGAVADTISQ 27  
DB 6 MLKKGITVALHAGKAAALGAAADTISQ 31

RESULT 3  
US-09-181-941-7  
; Sequence 7, Application US/09181941  
; Patent No. 6440690  
; GENERAL INFORMATION:  
; APPLICANT: Mor, Amram  
; APPLICANT: Vouldoukis, Ioannis  
; APPLICANT: Nicolas, Pierre  
; TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION  
; TITLE OF INVENTION: OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/181,941  
; FILING DATE: 28-Oct-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/574,701  
; FILING DATE: 19-DEC-1995

APPLICATION NUMBER: FR 95 07831  
FILING DATE: 29-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 3909-0021-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6440690e  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-181-941-7

Query Match 85.9%; Score 110; DB 4; Length 34;  
Best Local Similarity 84.6%; Pred. No. 5.9e-11;  
Matches 22; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VLKKGITVALHAGKAAALGAVADTISQ 27  
DB 6 MLKKGITVALHAGKAAALGAAADTISQ 31

RESULT 4  
US-09-181-941-8  
; Sequence 8, Application US/09181941  
; Patent No. 6440690  
; GENERAL INFORMATION:  
; APPLICANT: Mor, Amram  
; APPLICANT: Vouldoukis, Ioannis  
; APPLICANT: Nicolas, Pierre  
; TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION  
; TITLE OF INVENTION: OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/181,941  
; FILING DATE: 28-Oct-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/574,701  
; FILING DATE: 19-DEC-1995  
; APPLICATION NUMBER: FR 95 07831  
; FILING DATE: 29-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 3909-0021-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-493-4935  
; TELEFAX: 650-493-5556  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 amino acids  
TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6440690e  
SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-09-181-941-8

Query Match 82.0%; Score 105; DB 4; Length 34;  
Best Local Similarity 80.8%; Pred. No. 3.7e-10;  
Matches 21; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 VLKKGITVALHAGKALGAAVADTISQ 27  
DB 6 MLKKGITVALHAGKALGAAVADTISQ 31

RESULT 5  
US-09-030-619-201  
; Sequence 201, Application US/09030619B  
; Patent No. 6503881  
; GENERAL INFORMATION:  
; APPLICANT: Krieger, Timothy J.  
; APPLICANT: Taylor, Robert  
; APPLICANT: Erfile, Douglas  
; APPLICANT: Fraser, Janet R.  
; APPLICANT: West, Michael H.P.  
; APPLICANT: McNicol, Patricia J.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING  
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION  
; TITLE OF INVENTION: WITH ANTIBIOTICS  
; FILE REFERENCE: 660081.406  
; CURRENT APPLICATION NUMBER: US/09/030,619B  
; CURRENT FILING DATE: 1998-02-25  
; NUMBER OF SEQ ID NOS: 232  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 201  
; LENGTH: 32  
; TYPE: PRT  
; ORGANISM: Phyllomedusa sauvagii  
US-09-030-619-201

Query Match 77.7%; Score 99.5; DB 4; Length 32;  
Best Local Similarity 84.6%; Pred. No. 2.6e-09;  
Matches 22; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 2 VLKKGITVALHAGKALGAAVADTISQ 27  
DB 6 MLKKGITVALHAGKALGAAVADTISQ 30

RESULT 6  
US-09-181-941-16  
; Sequence 16, Application US/09181941  
; Patent No. 6440690  
; GENERAL INFORMATION:  
; APPLICANT: Mor, Amram  
; APPLICANT: Vouldoukis, Ioannis  
; APPLICANT: Nicolas, Pierre  
; TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION  
; TITLE OF INVENTION: OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSEQ for Windows Version 2.0b  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/181,941  
FILING DATE: 28-Oct-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/574,701  
FILING DATE: 19-DEC-1995  
APPLICATION NUMBER: FR 95 07831  
FILING DATE: 29-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 3909-0021-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-09-181-941-16

Query Match 57.0%; Score 73; DB 4; Length 19;  
Best Local Similarity 93.8%; Pred. No. 2.5e-05;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 HAGKALGAAVADTISQ 27  
DB 1 HAGKALGAAVADTISQ 16

RESULT 7  
US-09-143-124-20  
; Sequence 20, Application US/09143124  
; Patent No. 6288212  
; GENERAL INFORMATION:  
; APPLICANT: Hancock, Robert E. W.  
; APPLICANT: Gough, Monisha A.  
; APPLICANT: Patrzykat, Aleksander  
; APPLICANT: Woods, Donald  
; APPLICANT: Jia, Xiaoyan  
; TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC  
; TITLE OF INVENTION: PEPTIDES AND METHODS OF USE THEREFOR  
; FILE REFERENCE: 07422/016001  
; CURRENT APPLICATION NUMBER: US/09/143,124  
; CURRENT FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 30  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antimicrobial cationic peptide  
US-09-143-124-20

Query Match 46.1%; Score 59; DB 3; Length 30;  
Best Local Similarity 61.9%; Pred. No. 0.0074;  
Matches 13; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 VLKKGITVALHAGKALGAAV 22  
DB 6 MLKKAHVGVKGVKALGAAA 26

RESULT 8  
US-09-181-941-11  
; Sequence 11, Application US/09181941  
; Patent No. 6440690  
; GENERAL INFORMATION:

```
; APPLICANT: Mor, Amram
; Vouldoukis, Ioannis
; Nicolas, Pierre
; TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION
; OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/181,941
; FILING DATE: 28-Oct-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/574,701
; FILING DATE: 19-DEC-1995
; APPLICATION NUMBER: PR 95 07831
; FILING DATE: 29-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 3909-0021-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5536
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6440690e
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-181-941-11
Query Match 43.0%; Score 55; DB 4; Length 18;
Best Local Similarity 76.9%; Pred. No. 0.018;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 VLKKIGTVALHAG 14
; :|||:|||||
Db 6 MLKKIGTVALHAG 18

RESULT 9
US-09-143-124-19
; Sequence 19, Application US/09143124
; Patent No. 6288212
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Gough, Monisha A.
; APPLICANT: Patrzykat, Aleksander
; APPLICANT: Woods, Donald
; APPLICANT: Jia, Xiaoyan
; TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC
; FILE REFERENCE: 07422/016001
; CURRENT APPLICATION NUMBER: US/09/143,124
; CURRENT FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antimicrobial cationic peptide
US-09-143-124-21
Query Match 42.2%; Score 54; DB 3; Length 29;
Best Local Similarity 63.2%; Pred. No. 0.045;
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 KKIGTVALHAGKAAALGAVA 22
; |||:|||||
Db 7 KKAHVGVKHKVKAALGAAA 25

RESULT 10
US-09-143-124-21
; Sequence 21, Application US/09143124
; Patent No. 6288212
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Gough, Monisha A.
; APPLICANT: Patrzykat, Aleksander
; APPLICANT: Woods, Donald
; APPLICANT: Jia, Xiaoyan
; TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC
; FILE REFERENCE: 07422/016001
; CURRENT APPLICATION NUMBER: US/09/143,124
; CURRENT FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antimicrobial cationic peptide
US-09-143-124-21
Query Match 42.2%; Score 54; DB 3; Length 29;
Best Local Similarity 63.2%; Pred. No. 0.045;
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 KKIGTVALHAGKAAALGAVA 22
; |||:|||||
Db 7 KKAHVGVKHKVKAALGAAA 25

RESULT 11
US-09-181-941-14
; Sequence 14, Application US/09181941
; Patent No. 6440690
; GENERAL INFORMATION:
; APPLICANT: Mor, Amram
; Vouldoukis, Ioannis
; Nicolas, Pierre
; TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION
; OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/143,124
; FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 29
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antimicrobial cationic peptide
US-09-143-124-19
Query Match 42.2%; Score 54; DB 3; Length 29;
Best Local Similarity 63.2%; Pred. No. 0.045;
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 KKIGTVALHAGKAAALGAVA 22
; |||:|||||
Db 7 KKAHVGVKHKVKAALGAAA 25

RESULT 10
US-09-143-124-21
; Sequence 21, Application US/09143124
; Patent No. 6288212
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Gough, Monisha A.
; APPLICANT: Patrzykat, Aleksander
; APPLICANT: Woods, Donald
; APPLICANT: Jia, Xiaoyan
; TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC
; FILE REFERENCE: 07422/016001
; CURRENT APPLICATION NUMBER: US/09/143,124
; CURRENT FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antimicrobial cationic peptide
US-09-143-124-21
Query Match 42.2%; Score 54; DB 3; Length 29;
Best Local Similarity 63.2%; Pred. No. 0.045;
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 KKIGTVALHAGKAAALGAVA 22
; |||:|||||
Db 7 KKAHVGVKHKVKAALGAAA 25

RESULT 11
US-09-181-941-14
; Sequence 14, Application US/09181941
; Patent No. 6440690
; GENERAL INFORMATION:
; APPLICANT: Mor, Amram
; Vouldoukis, Ioannis
; Nicolas, Pierre
; TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION
; OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
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Patent No. 640690  
GENERAL INFORMATION:  
APPLICANT: Mor, Amram  
Vouldoukis, Ioannis

```

1  RESULT 14
2  PCT-US95-04589-107
3  ; Sequence 107, Application PC/TUS9504589
4  ; GENERAL INFORMATION:
5  ; APPLICANT: Ausubel, Frederick M.
6  ; APPLICANT: Staskawicz, Brian J.
7  ; APPLICANT: Brent, Andrew P.
8  ; APPLICANT: Dahlbeck, Douglas
9  ; APPLICANT: Katagiri, Fumaki
10 ; APPLICANT: Kunkel, Barbara N.
11 ; APPLICANT: Mindrinos, Michael N.
12 ; APPLICANT: Yu, Guo-Liang
13 ; TITLE OF INVENTION: RS2 GENE AND USES THEREOF
14 ; NUMBER OF SEQUENCES: 201
15 ; CORRESPONDENCE ADDRESS:
16 ; ADDRESS: Fish & Richardson
17 ; STREET: 225 Franklin Street Suite 3100
18 ; CITY: Boston
19 ; STATE: MA
20 ; COUNTRY: USA
21 ; ZIP: 02110-2904

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COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04589  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,360  
FILING DATE: 13-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00786/230001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 100254  
INFORMATION FOR SEQ ID NO: 107:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1209 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-04589-107

Query Match 37.5%; Score 48; DB 5; Length 1209;  
Best Local Similarity 46.4%; Pred. No. 32;  
Matches 13; Conservative 4; Mismatches 9; Indels 2; Gaps 2;  
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Db 142 DALKKVGLKGHWIGKNDKQGAIAADKVS 169

RESULT 15  
US-08-310-912A-107  
Sequence 107, Application US/08310912A  
Patent No. 5981730  
GENERAL INFORMATION:  
APPLICANT: Ausubel, Frederick M.  
APPLICANT: Staskawicz, Brian J.  
APPLICANT: Brent, Andrew F.  
APPLICANT: Dahlbeck, Douglas  
APPLICANT: Katagiri, Fumiaki  
APPLICANT: Kunkel, Barbara N.  
APPLICANT: Mindrinos, Michael N.  
APPLICANT: Yu, Guo-Liang  
TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 208  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2904  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/310,912A  
FILING DATE: September 22, 1994  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/227,360  
FILING DATE: April 13, 1994

ATTORNEY/AGENT INFORMATION:  
NAME: Lech, Karen F.  
REGISTRATION NUMBER: 35,238  
REFERENCE/DOCKET NUMBER: 00786/254001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 100254  
INFORMATION FOR SEQ ID NO: 107:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1258 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-310-912A-107  
Query Match 37.5%; Score 48; DB 2; Length 1258;  
Best Local Similarity 46.4%; Pred. No. 34;  
Matches 13; Conservative 4; Mismatches 9; Indels 2; Gaps 2;  
Qy 1 DVLKKIGTV-ALHAGK-AALGAVADTIS 26  
Db 191 DALKKVGLKGHWIGKNDKQGAIAADKVS 218  
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Job time : 21 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 10, 2003, 20:24:16 / Search time 42 seconds  
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102.039 Million cell updates/sec

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Perfect score: 128

Sequence: 1 DVLKIGTVALHAGRAALGAVADTISQ 27

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Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	128	100.0	27	21	AA18725 Amino acid sequenc
2	128	100.0	31	21	AA18726 Amino acid sequenc
3	128	100.0	31	21	AA12436 Dermaseptin B amin
4	128	100.0	32	21	AA18748 A mature dermasapt
5	128	100.0	78	21	AA18724 A dermasaptin prec
6	110	85.9	33	21	AA18730 Cationic antimicro
7	110	85.9	33	23	AAU90985 Transplant media a
8	110	85.9	34	21	AA18732 Amino acid sequenc
9	110	85.9	34	22	AA18732 Antimicrobial pept

10	110	85.9	34	24	AAE34434 Frog dermasaptin p
11	105	82.0	34	21	AA18733 Amino acid sequenc
12	105	82.0	34	23	AAU90986 Transplant media a
13	99.5	77.7	32	19	AAW6438 Cationic peptide d
14	99.5	77.7	32	21	AAU91737 Cationic peptide d
15	99.5	77.7	32	24	ABU59614 Cationic cancer -t
16	59	46.1	30	21	AAU87377 Cationic antimicro
17	54.5	42.6	417	16	AAE6223 Cystathionine gamm
18	54	42.2	29	21	AAU87376 Cationic antimicro
19	54	42.2	29	21	AAU87378 Cationic antimicro
20	51.5	40.2	31	21	AA18728 Amino acid sequenc
21	50	39.1	30	21	AA18731 Human liver peptid
22	49	38.3	287	22	ABG49743 Peptide #2384 enco
23	49	38.3	287	22	ABG29733 Peptide #2384 enco
24	49	38.3	287	22	AAU55715 Human brain expres
25	49	38.3	287	22	AAU68093 Human bone marrow
26	49	38.3	287	22	AAU15917 Peptide #2351 enco
27	49	38.3	287	22	AAU03653 Peptide #2335 enco
28	48.5	37.9	30	21	AA18734 Amino acid sequenc
29	48.5	37.9	30	23	AAU90987 Transplant media a
30	48.5	37.9	36	21	AA18727 Amino acid sequenc
31	48	37.5	171	22	AAU16272 Human novel secret
32	48	37.5	171	24	AAU55341 Human novel polype
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34	48	37.5	723	21	AAU75477 Neisseria meningit
35	48	37.5	1274	22	AAU79202 Corynebacterium gl
36	48	37.5	1295	22	AAU92726 C glutamicum prote
37	47.5	37.1	590	23	AAE17085 Arabidopsis thalia
38	47.5	37.1	642	23	AAE17088 Arabidopsis thalia
39	47	36.7	29	23	AAU90994 Transplant media a
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42	47	36.7	391	24	ABF77997 N. gonorrhoeae ami
43	47	36.7	403	7	AAU60274 Sequence of creati
44	47	36.7	403	9	AAU90680 Creatine amidohydr
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ALIGNMENTS

RESULT 1  
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ID AA18725 standard; Protein; 27 AA.

XX AA18725;

AC AA18725;

XX 22-JAN-2001 (first entry)

XX Amino acid sequence of mature protein dermasaptin b.

XX Dermaseptin; antibacterial; fungal growth; temporin; transgenic plant;

XX cationic peptide; pathogen resistance.

XX Phyllomedusa bicolor.

XX WO20005337-A1.

XX 21-SEP-2000.

XX 16-MAR-2000; 2000WO-CA00288.

XX 17-MAR-1999; 99US-0125072.

XX (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.

XX Misra S, Kay WD;

XX WPI; 2000-647077/t2.

XX Transgenic plants resistant to broad spectrum of pathogens useful for  
PT producing biologically active cationic peptides, comprises nucleic acid  
PT molecule encoding temporin and/or dermasaptin peptides

XX PS Claim 3; Page 47; 58pp; English.

XX CC AAB18725-36 represent mature processed forms of dermaseptin. Dermaseptin

XX CC has antibacterial activity, and inhibits fungal growth. Cationic

XX CC peptides derived from temporins and dermaseptins are used to produce

XX CC transgenic plants. The transgenic plants are useful for producing

XX CC biologically active cationic peptides such as temporins and dermaseptins

XX CC in large quantities. The peptide confers broad spectrum pathogen

XX CC resistance including enhanced resistance to both fungal and bacterial

XX CC pathogens in the transgenic plants. The transgenic plants may be used

XX CC in conventional agricultural applications such as food crops, medical

XX CC and other applications.

XX SQ Sequence 27 AA;

Query Match 100.0%; Score 128; DB 21; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.1e-12;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVLKKIGTVALHAGKAALGAVADTISQ 27  
Db 1 DVLKKIGTVALHAGKAALGAVADTISQ 27

RESULT 2

AAB18726

ID AAB18726 standard; Protein; 31 AA.

XX AC AAB18726;

XX DT 22-JAN-2001 (first entry)

XX -DE Amino acid sequence of mature protein dermaseptin B.

XX KW Dermaseptin; antibacterial; fungal growth; temporin; transgenic plant;

XX KW cationic peptide; pathogen resistance.

XX -OS Phylomedusa bicolor.

XX XX WO20005337-A1.

XX PD 21-SEP-2000.

XX PF 16-MAR-2000; 2000WO-CA00288.

XX PR 17-MAR-1999; 99US-0125072.

XX PA (UVVI-) UNIV VICTORIA INNOVATION & DEV CORP.

XX PI Misra S; Kay WD;

XX XX WPI; 2000-647077/62.

XX PT Transgenic plants resistant to broad spectrum of pathogens useful for

XX PT producing biologically active cationic peptides, comprises nucleic acid

XX PT molecule encoding temporin and/or dermaseptin peptides -

XX PS Claim 3; Page 47; 58pp; English.

XX CC AAB18725-36 represent mature processed forms of dermaseptin. Dermaseptin

XX CC has antibacterial activity, and inhibits fungal growth. Cationic

XX CC peptides derived from temporins and dermaseptins are used to produce

XX CC transgenic plants. The transgenic plants are useful for producing

XX CC biologically active cationic peptides such as temporins and dermaseptins

XX CC in large quantities. The peptide confers broad spectrum pathogen

XX CC resistance including enhanced resistance to both fungal and bacterial

XX CC pathogens in the transgenic plants. The transgenic plants may be used

XX CC in conventional agricultural applications such as food crops, medical

XX CC and other applications.

XX SQ Sequence 31 AA;

Query Match 100.0%; Score 128; DB 21; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.1e-12;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVLKKIGTVALHAGKAALGAVADTISQ 27  
Db 1 DVLKKIGTVALHAGKAALGAVADTISQ 27

RESULT 2

AAB18726

ID AAB18726 standard; Protein; 31 AA.

XX AC AAB18726;

XX DT 22-JAN-2001 (first entry)

XX -DE Amino acid sequence of mature protein dermaseptin B.

XX KW Dermaseptin; antibacterial; fungal growth; temporin; transgenic plant;

XX KW cationic peptide; pathogen resistance.

XX -OS Phylomedusa bicolor.

XX XX WO20005337-A1.

XX PD 21-SEP-2000.

XX PF 16-MAR-2000; 2000WO-CA00288.

XX PR 17-MAR-1999; 99US-0125072.

XX PA (UVVI-) UNIV VICTORIA INNOVATION & DEV CORP.

XX PI Misra S; Kay WD;

XX XX WPI; 2000-647077/62.

XX PT Transgenic plants resistant to broad spectrum of pathogens useful for

XX PT producing biologically active cationic peptides, comprises nucleic acid

XX PT molecule encoding temporin and/or dermaseptin peptides -

XX PS Claim 3; Page 47; 58pp; English.

XX CC AAB18725-36 represent mature processed forms of dermaseptin. Dermaseptin

XX CC has antibacterial activity, and inhibits fungal growth. Cationic

XX CC peptides derived from temporins and dermaseptins are used to produce

XX CC transgenic plants. The transgenic plants are useful for producing

XX CC biologically active cationic peptides such as temporins and dermaseptins

XX CC in large quantities. The peptide confers broad spectrum pathogen

XX CC resistance including enhanced resistance to both fungal and bacterial

XX CC pathogens in the transgenic plants. The transgenic plants may be used

XX CC in conventional agricultural applications such as food crops, medical

XX CC and other applications.

XX SQ Sequence 31 AA;

Query Match 100.0%; Score 128; DB 21; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.1e-12;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVLKKIGTVALHAGKAALGAVADTISQ 27  
Db 1 DVLKKIGTVALHAGKAALGAVADTISQ 31

RESULT 4

AAB18748

ID AAB18748 standard; Protein; 32 AA.

XX AC AAB18748;

XX DT 22-JAN-2001 (first entry)

XX XX

Query Match 100.0%; Score 128; DB 21; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.3e-12;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVLKKIGTVALHAGKAALGAVADTISQ 27  
Db 5 DVLKKIGTVALHAGKAALGAVADTISQ 31

RESULT 3

AAB12436

ID AAB12436 standard; peptide; 31 AA.

XX AC AAB12436;

XX DT 20-OCT-2000 (first entry)

XX DE Dermaseptin B amino acid sequence.

XX KW CEMA; Pro-CEMA; dermaseptin B; temporin A; cecropin A; melittin;

XX KW Cema 35S promoter; cationic polypeptide; antimicrobe; transgenic plant;

XX KW expression vector; agrobacillus; callus; phytopathogen; bacteria;

XX KW fungus; calli; antifungal; antibacterial.

XX OS Unidentified.

XX XX CN1249310-A.

XX PD 05-APR-2000.

XX PF 28-SEP-1998; 98CN-0112269.

XX PR 28-SEP-1998; 98CN-0112269.

XX PA (ZHOU/) ZHOU G.

XX XX Zhou G;

XX XX WPI; 2000-400710/35.

XX PT Cationic polypeptide process for expressing antimicrobe in plant -

XX PS Claim 2; Page 1; 7pp; Chinese.

XX CC The present invention describes a transgenic plant expression vector

XX CC containing three antimicrobe cationic polypeptides. The plant tissue is

XX CC introduced to these genes via agrobacillus and in the callus culture,

XX CC the callus resisting phytopathogen (bacteria and fungus) can be

XX CC externally chosen. Choosing these calli can regenerate plants and

XX CC directly test its antifungal and antibacterial powder. After these

XX CC transgenic plants are ripened, whole or partial plant can be harvested.

XX CC The present sequence represents a specifically claimed peptide from

XX CC the present invention.

XX SQ Sequence 31 AA;

Query Match 100.0%; Score 128; DB 21; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.3e-12;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVLKKIGTVALHAGKAALGAVADTISQ 27  
Db 5 DVLKKIGTVALHAGKAALGAVADTISQ 31

RESULT 4

AAB18748

ID AAB18748 standard; Protein; 32 AA.

XX AC AAB18748;

XX DT 22-JAN-2001 (first entry)

XX XX

DE A mature dermaseptin protein with a N-terminal extension.

XX Dermaseptin; antibacterial; fungal growth; temporin; transgenic plant;  
KW cationic peptide; pathogen resistance.

XX Synthetic.  
OS Phyllomedusa bicolor.

XX WO200055337-A1.

XX 21-SEP-2000.

XX 16-MAR-2000; 2000WO-CA00288.

XX 17-MAR-1999; 99US-0125072.

XX (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.

XX Misra S, Kay WD;

XX WPI; 2000-647077/62.

XX N-PSDB; AAA75751.

XX Transgenic plants resistant to broad spectrum of pathogens useful for  
PT producing biologically active cationic peptides, comprises nucleic acid  
PT molecule encoding temporin and/or dermaseptin peptides

XX Example; Page 51; 58pp; English.

XX The present sequence represents a mature dermaseptin polypeptide  
CC which has a N-terminal extension. Dermaseptin has antibacterial  
CC activity, and inhibits fungal growth. Cationic peptides derived from  
CC temporins and dermaseptins are used to produce transgenic plants. The  
CC transgenic plants are useful for producing biologically active cationic  
CC peptides such as temporins and dermaseptins in large quantities. The  
CC peptide confers broad spectrum pathogen resistance including enhanced  
CC resistance to both fungal and bacterial pathogens in the transgenic  
CC plants. The transgenic plants may be used in conventional agricultural  
CC applications such as food crops, medical and other applications.

XX Sequence 32 AA;

Query Match 100.0%; Score 128; DB 21; Length 32;

Best Local Similarity 100.0%; Pred. No. 1.3e-12;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVLKKGITVALHAGKAALGAVADTISQ 27

Db 6 DVLKKGITVALHAGKAALGAVADTISQ 32

RESULT 5

AAB18724

ID AAB18724 standard; Protein; 78 AA.

XX

XX AAB18724;

XX

DT 22-JAN-2001 (first entry)

XX

DE A dermaseptin precursor polypeptide.

XX

KW Dermaseptin; antibacterial; fungal growth; temporin; transgenic plant;

XX

KW cationic peptide; pathogen resistance.

XX

OS Phyllomedusa bicolor.

XX

XX WO200055337-A1.

XX

PD 21-SEP-2000.

XX

XX 16-MAR-2000; 2000WO-CA00288.

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PR 17-MAR-1999; 99US-0125072.

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(UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.

XX Misra S, Kay WD;

XX WPI; 2000-647077/62.

XX N-PSDB; AAA75749.

XX Transgenic plants resistant to broad spectrum of pathogens useful for  
PT producing biologically active cationic peptides, comprises nucleic acid  
PT molecule encoding temporin and/or dermaseptin peptides

XX Disclosure; Page 47; 58pp; English.

XX The present sequence represents a dermaseptin precursor polypeptide.  
CC The precursor is processed to produce two mature forms, dermaseptin b  
CC (AAB18724) and dermaseptin B (AAB18726). Dermaseptin has antibacterial  
CC activity, and inhibits fungal growth. Cationic peptides derived from  
CC temporins and dermaseptins are used to produce transgenic plants. The  
CC transgenic plants are useful for producing biologically active cationic  
CC peptides such as temporins and dermaseptins in large quantities. The  
CC peptide confers broad spectrum pathogen resistance including enhanced  
CC resistance to both fungal and bacterial pathogens in the transgenic  
CC plants. The transgenic plants may be used in conventional agricultural  
CC applications such as food crops, medical and other applications.

XX Sequence 78 AA;

Query Match 100.0%; Score 128; DB 21; Length 78;

Best Local Similarity 100.0%; Pred. No. 3.6e-12;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVLKKGITVALHAGKAALGAVADTISQ 27

Db 49 DVLKKGITVALHAGKAALGAVADTISQ 75

RESULT 6

AAY87380

ID AAY87380 standard; peptide; 33 AA.

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XX AAY87380;

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Cationic antimicrobial peptide DER (frog dermaseptin), SEQ ID NO.23.

XX Antimicrobial; cationic; antibacterial; antiproliferative;  
KW endotoxaemia; sepsis; wound repair; tissue regeneration;  
KW transgenic animal; pathogen resistance.

XX Anura.

XX WO200012528-A1.

XX 09-MAR-2000.

XX 27-AUG-1999; 99WO-US19646.

XX 28-AUG-1998; 98US-0143124.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX Hancock RW, Gough MA, Patrzykat A, Woods D, Jia X;

XX WPI; 2000-270790/23.

XX Novel anti-endotoxic, antimicrobial cationic peptides useful for  
PT inhibiting endotoxaemia/sepsis-associated disorder or cell  
PT proliferation, accelerating wound healing, and treating respiratory  
PT associated disorder

XX Claim 17; Page 93; 116pp; English.

XX CC The invention relates to a novel class of cationic antimicrobial  
 CC peptides (AAV87358-Y87361 and AAV87383-Y87391). It also encompasses  
 CC nucleotides encoding the peptides and a transgenic animal comprising a  
 CC nucleotide sequence encoding an anti-microbial peptide. The cationic  
 CC antimicrobial peptides of the invention are useful for inhibiting the  
 CC growth of Gram positive or Gram negative bacteria, in combination with an  
 CC antibiotic or lysozyme. The peptides are also useful for inhibiting the  
 CC growth of a eukaryotic cell e.g., a neoplastic cell, and sequences  
 CC AAV87358-Y87369 may be used for inhibiting cell proliferation-associated  
 CC disorders such as cancer. Peptides AAV87360-Y87369 are useful for  
 CC inhibiting endotoxaemia or a sepsis-associated disorder such as septic  
 CC shock. The peptides of the invention may also be used for accelerating  
 CC wound repair in a patient when coadministered with a healing agent such  
 CC as TGF-beta (transforming growth factor-beta). The peptides are used for  
 CC treating a respiratory or pulmonary-associated infection, or a disorder  
 CC such as cystic fibrosis. The peptides are used for revitalising scar  
 CC tissue, for wound repair. The peptides are used for revitalising scar  
 CC and for promoting tissue growth in skin grafts. Nucleic acids encoding  
 CC peptides AAV87372-Y87378 and AAV87383-Y87391 may be used in the  
 CC generation of transgenic animals, with nucleotide encoding sequences  
 CC AAV87372 and AAV87374-Y87378 being particularly useful for the generation  
 CC of transgenic fish with enhanced resistance to pathogenic organisms.  
 CC Sequences AAV87358-Y87361 and AAV87383-Y87391 represent cationic  
 CC antimicrobial peptides claimed for use in various embodiments of the  
 CC invention.

XX SQ Sequence 33 AA;

Query Match 85.9%; Score 110; DB 21; Length 33;  
 Best Local Similarity 84.6%; Pred. No. 8e-10; Indels 0; Gaps 0;  
 Matches 22; Conservative 3; Mismatches 1;

\*QY 2 VLKKGITVALHAGKAAALGAAVADTISQ 27  
 Db :|||:|||||  
 6 MLKKLGTWALHAGKAAALGAAADTISQ 31

# RESULT 7

AAU90985  
 ID AAU90985 standard; Peptide; 33 AA.

AC AAU90985;

DT 05-JUN-2002 (first entry)

DE Transplant media associated antimicrobial peptide #21.

KW Transplant; antimicrobial peptide; pore forming agent;  
 KW cell surface receptor binding compound; kidney transplant;  
 KW cardioplegia; organ transplant; transplant rejection.

XX Phyllomedusa sauvagel.

OS WO200209738-A1.

FN 07-FEB-2002.

XX 27-JUL-2001; 2001WO-US23785.

XX 28-JUL-2000; 2000US-221632P.

PR 17-NOV-2000; 2000US-249602P.

PR 15-MAY-2001; 2001US-290932P.

XX (MURP/) MURPHY C J.

XX Murphy CJ, Reid TW, Mcanulty JF;

XX WPI; 2002-268995/31.

XX Media comprising antimicrobial polypeptides or pore forming agents  
 PT and/or cell surface receptor binding compounds useful for the storage  
 PT and preservation of organs prior to transplant -

XX

PS Disclosure; Page 26; 78pp; English.

CC The invention describes new transplant compositions comprising  
 CC antimicrobial polypeptides or pore forming agents and/or cell surface  
 CC receptor binding compounds. The media is capable of extending the  
 CC preservation period past 72 hours and can provide organs with increased  
 CC functionality upon transplant. Animals receiving kidneys stored in the  
 CC media of the present invention for either three or four days had serum  
 CC creatinine levels of less than half of those observed in control animals  
 CC receiving kidneys stored in UW solution (defined in the specification)  
 CC alone. Lower serum creatinine levels are indicative of healthier kidneys  
 CC and a more preferable prognosis for the transplant patient. The media of  
 CC the invention are useful for decreasing the incidence and/or severity of  
 CC delayed graft function in patients receiving transplanted kidneys stored  
 CC and/or treated in the media. The media may also be used in procedures  
 CC such as cardioplegia. It is contemplated that transplant of healthier  
 CC organs leads to a decrease in chronic rejection. This sequence represents  
 CC an antimicrobial peptide studied in the development of the transplant  
 CC media.

SQ Sequence 33 AA;

Query Match 85.9%; Score 110; DB 23; Length 33;  
 Best Local Similarity 84.6%; Pred. No. 8e-10; Indels 0; Gaps 0;  
 Matches 22; Conservative 3; Mismatches 1;

QY 2 VLKKGITVALHAGKAAALGAAVADTISQ 27  
 Db :|||:|||||  
 6 MLKKLGTWALHAGKAAALGAAADTISQ 31

# RESULT 8

AAI8732  
 ID AAI8732 standard; Protein; 34 AA.

AC AAI8732;

DT 22-JAN-2001 (first entry)

DE Amino acid sequence of a mature processed form of dermaseptin.

XX Dermaseptin; antibacterial; fungal growth; temporin; transgenic plant;  
 KW cationic peptide; pathogen resistance.

XX Phyllomedusa sauvagel.

XX WO200005337-A1.

XX 21-SEP-2000.

XX 16-MAR-2000; 2000WO-CA00288.

XX 17-MAR-1999; 99US-0125072.

XX (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.

XX Misra S, Kay WD;

XX WPI; 2000-647077/62.

XX Transgenic plants resistant to broad spectrum of pathogens useful for  
 PT producing biologically active cationic peptides, comprises nucleic acid  
 PT molecule encoding temporin and/or dermaseptin peptides -

XX Claim 3; Page 49; 58pp; English.

XX AAI8725-36 represent mature processed forms of dermaseptin. Dermaseptin  
 CC has antibacterial activity, and inhibits fungal growth. Cationic  
 CC peptides derived from temporins and dermaseptins are used to produce  
 CC transgenic plants. The transgenic plants are useful for producing  
 CC biologically active cationic peptides such as temporins and dermaseptins  
 CC in large quantities. The peptide confers broad spectrum pathogen

CC resistance including enhanced resistance to both fungal and bacterial  
 CC pathogens in the transgenic plants. The transgenic plants may be used  
 CC in conventional agricultural applications such as food crops, medical  
 CC and other applications.

SQ Sequence 34 AA;  
 Query Match 85.9%; Score 110; DB 21; Length 34;  
 Best Local Similarity 84.6%; Pred. No. 8.3e-10;  
 Matches 22; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 VLKKGITVALHAGKAALGAVADTISQ 27  
 :|||:|||||  
 Db 6 MLKKGITVALHAGKAALGAAADTISQ 31

RESULT 9  
 AAB91864  
 ID AAB91864 standard; Peptide; 34 AA.

XX AC AAB91864;  
 DT 22-JUN-2001 (first entry)  
 DE Antimicrobial peptide SEQ ID NO:1040.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;  
 KW blood component; modification; succinimide; maleimido group; amino;  
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.  
 OS Synthetic.

XX WO200069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US13576.

XX 17-MAY-1999; 99US-0134406.

XX 10-SEP-1999; 99US-0153406.

XX 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibautau K;

XX WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents

XX peptidase degradation, useful for increasing length of in vivo activity

XX Disclosure; Page 536; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)  
 CC comprising a therapeutically active amino acid region (III) and a  
 CC reactive group (II) (e.g. succinimide and maleimido groups) attached to  
 CC a less therapeutically active amino acid region (IV), which covalently  
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
 CC factors and neurotransmitters, to protect them from peptidase activity  
 CC in vivo for the treatment of various disorders. Endogenous therapeutic  
 CC peptides are not suitable as drug candidates as they require frequent  
 CC administration due to rapid degradation by peptidases in the body.  
 CC Modifying and attaching therapeutic peptides to albumin prevents or  
 CC reduces the action of peptidases to increase length of activity (half  
 CC life) and specificity as bonding to large molecules decreases  
 CC intracellular uptake and interference with physiological processes.  
 CC AAB90829 to AAB92441 represent peptides which can be used in the  
 CC exemplification of the present invention.

XX

SQ Sequence 34 AA;

Query Match 85.9%; Score 110; DB 22; Length 34;  
 Best Local Similarity 84.6%; Pred. No. 8.3e-10;  
 Matches 22; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 VLKKGITVALHAGKAALGAVADTISQ 27  
 :|||:|||||  
 Db 6 MLKKGITVALHAGKAALGAAADTISQ 31

RESULT 10  
 AAE34434  
 ID AAE34434 standard; peptide; 34 AA.

XX AAE34434;

DT 14-MAY-2003 (first entry)

DE Frog dermaseptin peptide.

XX Antimicrobial; purple blotch; gene therapy; antibacterial; fungicide;  
 KW frog; dermaseptin.

XX Rana sp.

XX WO200295076-A2.

XX 28-NOV-2002.

XX 17-MAY-2002; 2002WO-JP04800.

XX 23-MAY-2001; 2001JP-0154321.

XX 26-DEC-2001; 2001JP-0394821.

XX (TOYU) TOYOTA CHUO KENYUSHO KK.

XX Muramoto N, Imaeda T, Hirai M, Shimamura T;

XX WPI; 2003-156762/15.

XX New polypeptide comprising at least one protease-resistant or  
 PT protease-sensitive sequence, bound to the C-terminal side of the target  
 PT polypeptide, useful as antimicrobial agent against Ceratocystis  
 PT fimbriata, or Escherichia coli -

XX Example 14; Fig 5; 50pp; English.

XX The invention relates to a polypeptide comprising at least one protease-  
 CC resistant or protease-sensitive sequence, bound to the C-terminal side  
 CC of the target polypeptide. The polypeptides are useful as antimicrobial  
 CC agents against Ceratocystis fimbriata, which causes purple blotch in  
 CC sweet potatoes, or Escherichia coli. They are also used in gene therapy.  
 CC The present sequence is frog dermaseptin peptide used in the  
 CC exemplification of the invention.

XX Sequence 34 AA;

Query Match 85.9%; Score 110; DB 24; Length 34;  
 Best Local Similarity 84.6%; Pred. No. 8.3e-10;  
 Matches 22; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 VLKKGITVALHAGKAALGAVADTISQ 27  
 :|||:|||||  
 Db 6 MLKKGITVALHAGKAALGAAADTISQ 31

RESULT 11

AAB18733  
 ID AAB18733 standard; Protein; 34 AA.

XX AAB18733;

XX

DT 22-JAN-2001 (first entry)  
 DE Amino acid sequence of a mature processed form of dermaseptin.  
 XX Dermaseptin; antibacterial; fungal growth; temporin; transgenic plant;  
 KW cationic peptide; pathogen resistance.  
 XX Phyllomedusa sauvagei.  
 XX WO200055337-A1.  
 XX 21-SEP-2000.  
 XX 16-MAR-2000; 2000WO-CA00288.  
 XX 17-MAR-1999; 99US-0135072.  
 XX (UUVI-) UNIV VICTORIA INNOVATION & DEV CORP.  
 PA Misra S, Kay WD;  
 PI WPI; 2000-647077/62.  
 XX Transgenic plants resistant to broad spectrum of pathogens useful for  
 PT producing biologically active cationic peptides, comprises nucleic acid  
 PT molecule encoding temporin and/or dermaseptin peptides -  
 XX Claim 3; Page 49; 58pp; English.  
 XX AAB18725-36 represent mature processed forms of dermaseptin. Dermaseptin  
 CC has antibacterial activity, and inhibits fungal growth. Cationic  
 CC peptides derived from temporins and dermaseptins are used to produce  
 CC transgenic plants. The transgenic plants are useful for producing  
 CC biologically active cationic peptides such as temporins and dermaseptins  
 CC in large quantities. The peptide confers broad spectrum pathogen  
 CC resistance including enhanced resistance to both fungal and bacterial  
 CC pathogens in the transgenic plants. The transgenic plants may be used  
 CC in conventional agricultural applications such as food crops, medical  
 CC and other applications.  
 XX Sequence 34 AA;  
 SQ Query Match 82.0%; Score 105; DB 21; Length 34;  
 Best Local Similarity 80.8%; Pred. No. 4.9e-09;  
 Matches 21; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 VLKKGITVALHAGKAAALGAVADTISQ 27  
 DB 6 MLKKLGTMALHAGKAAALGAAANTISQ 31  
 RESULT 12  
 ID AAU90986  
 AC AAU90986 standard; Peptide; 34 AA.  
 XX  
 DT 05-JUN-2002 (first entry)  
 XX Transplant media associated antimicrobial peptide #22.  
 DE Transplant; antimicrobial peptide; pore forming agent;  
 KW call surface receptor binding compound; kidney transplant;  
 KW cardioplegia; organ transplant; transplant rejection.  
 XX Phyllomedusa sauvagei.  
 XX WO200209738-A1.  
 XX 07-FEB-2002.  
 XX 27-JUL-2001; 2001WO-US23785.  
 XX

PR 28-JUL-2000; 2000US-221632P.  
 PR 17-NOV-2000; 2000US-249602P.  
 XX 15-MAY-2001; 2001US-290932P.  
 PA (MURP/) MURPHY C J.  
 XX Murphy CJ, Reid TW, Mcanulty JF;  
 XX WPI; 2002-268995/31.  
 XX Media comprising antimicrobial polypeptides or pore forming agents  
 PT and/or cell surface receptor binding compounds useful for the storage  
 PT and preservation of organs prior to transplant -  
 XX Disclosure; Page 26; 78pp; English.  
 XX The invention describes new transplant compositions comprising  
 CC antimicrobial polypeptides or pore forming agents and/or cell surface  
 CC receptor binding compounds. The media is capable of extending the  
 CC preservation period past 72 hours and can provide organs with increased  
 CC functionality upon transplant. Animals receiving kidneys stored in the  
 CC media of the present invention for either three or four days had serum  
 CC creatinine levels of less than half of those observed in control animals  
 CC receiving kidneys stored in UW solution (defined in the specification)  
 CC alone. Lower serum creatinine levels are indicative of healthier kidneys  
 CC and a more preferable prognosis for the transplant patient. The media of  
 CC the invention are useful for decreasing the incidence and/or severity of  
 CC delayed graft function in patients receiving transplanted kidneys stored  
 CC and/or treated in the media. The media may also be used in procedures  
 CC such as cardioplegia. It is contemplated that transplant of healthier  
 CC organs leads to a decrease in chronic rejection. This sequence represents  
 CC an antimicrobial peptide studied in the development of the transplant  
 CC media.  
 XX Sequence 34 AA;  
 SQ Query Match 82.0%; Score 105; DB 23; Length 34;  
 Best Local Similarity 80.8%; Pred. No. 4.9e-09;  
 Matches 21; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 VLKKGITVALHAGKAAALGAVADTISQ 27  
 DB 6 MLKKLGTMALHAGKAAALGAAANTISQ 31  
 RESULT 13  
 ID AAW66438  
 AC AAW66438 standard; peptide; 32 AA.  
 XX  
 DT 12-JAN-1999 (first entry)  
 XX Cationic peptide dermaseptin.  
 DE Indolicidin analogue; resistance; cationic peptide; antibiotic;  
 XX bacterial infection; tolerance; antibacterial; microorganism;  
 KW bacteria; fungus; parasite; virus.  
 XX Phyllomedusa sauvagei.  
 XX WO9840401-A2.  
 XX 17-SEP-1998.  
 XX 10-MAR-1998; 98WO-CA00190.  
 XX 25-FEB-1998; 98US-0030619.  
 PR 10-MAR-1997; 97US-0040649.  
 PR 20-AUG-1997; 97US-0915314.  
 PR 26-SEP-1997; 97US-0060099.  
 XX (MICK-) MICROLOGIX BIOTECH INC.  
 PA



XX Praser JR, McNicol PJ, West MHP;  
 XX WPI; 1998-520800/44.  
 XX New indolicidin peptide analogues - useful for, e.g. enhancing  
 XX activity of antibiotic or overcoming tolerance, acquired resistance  
 XX or inherent resistance of microorganisms  
 XX Disclosure; Page 10; 105pp; English.  
 XX  
 XX AAW66393 to AAW66469 represent native cationic peptides from the  
 XX present invention. The present invention describes compositions and  
 XX methods for treating infection, especially bacterial infections. The  
 XX compositions and methods use cationic peptides in combination with an  
 XX antibiotic agent which are then administered to a patient to enhance the  
 XX activity of the antibiotic agent, to overcome: (a) tolerance; (b)  
 XX acquired resistance; and (c) inherent resistance. The combinations of  
 XX antibiotics and cationic peptides can provide synergistic activity  
 XX against a microorganism that is tolerant, inherently resistant, or has  
 XX acquired resistance to an antibiotic agent. They can be used for killing  
 XX e.g. bacteria, fungi, parasites and viruses.  
 XX Sequence 32 AA;

Query Match 77.7%; Score 99.5; DB 19; Length 32;  
 Best Local Similarity 84.6%; Pred. No. 3.2e-08;  
 Matches 22; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 2 VLKKGTVLHAGKAAALGAVADTISQ 27  
 DB 6 MLKKGTMLHAGKAAALGA-ADTISQ 30

## RESULT 14

AY91737  
 ID AAY91737 standard; Peptide; 32 AA.

XX  
 AC AAY91737;

DT 06-JUN-2000 (first entry)

DE Cationic peptide Dermaseptin amino acid sequence.

XX Cationic peptide; tumour; pharmaceutical composition; cancer; treatment;  
 XX leukaemia; polyoxalkylene-modified; APO; lymphoma; multiple myeloma;  
 XX breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon;  
 XX multidrug resistance.

XX Unidentified.

XX WO9965506-A2.

XX 23-DEC-1999.

XX 14-JUN-1999; 99WO-CA00552.

XX 12-JUN-1998; 98US-0096541.

XX (MICR-) MICROLOGIX BIOTECH INC.

XX Friedland HD, Krieger TV, Taylor R, Erfle D, Fraser JR, West MHP;  
 XX WPI; 2000-223549/19.

XX Novel pharmaceutical composition containing optionally activated  
 XX polyoxalkylene-modified cationic peptides, useful for treating tumours

XX Disclosure; Page 11; 94pp; English.

XX This sequence represents a cationic peptide amino acid sequence, which  
 XX can be used in the pharmaceutical composition of the invention. The

CC invention relates to a pharmaceutical composition containing at least one  
 CC activated polyoxalkylene (APO)-modified cationic peptide. The  
 CC modification of peptides with APO increases their activity against tumour  
 CC cells, including those with a multidrug resistant phenotype. The  
 CC pharmaceutical composition can be used to treat tumours, specifically  
 CC lymphoma, leukaemia, multiple myeloma, or tumours of breast, lung, ovary,  
 CC cervix, uterus, skin, prostate, liver and colon.

XX Sequence 32 AA;

Query Match 77.7%; Score 99.5; DB 21; Length 32;  
 Best Local Similarity 84.6%; Pred. No. 3.2e-08;  
 Matches 22; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 2 VLKKGTVLHAGKAAALGAVADTISQ 27  
 DB 6 MLKKGTMLHAGKAAALGA-ADTISQ 30

## RESULT 15

ABU59614  
 ID ABU59614 standard; Peptide; 32 AA.

XX AC ABU59614;

XX 22-APR-2003 (first entry)

DE Cationic cancer -targeting peptide #46.

XX Targeting ligand; bioactive agent; polymer matrix; cancer; cytostatic;  
 XX cathepsin-D substrate; peptides; neuroreceptor; adrenal receptor;  
 XX fibronectin; vitronectin; integrin; RGD motif; angiogenic endothelium;  
 XX tumour; cationic cancer-targeting peptide.

XX Synthetic.

XX US2002041898-A1.

XX 11-APR-2002.

XX 25-JUL-2001; 2001US-0912609.

XX 05-JAN-2000; 2000US-0478124.

XX 31-OCT-2000; 2000US-0703474.

XX (UNGE/) UNGER E C.

XX (MATS/) MATSUNAGA T O.

XX (RAMA/) RAMASWAMI V.

XX (ROMA/) ROMANOWSKI M J.

XX Unger EC, Mateunaga TO, Ramaswami V, Romanowski MJ;

XX WPI; 2003-208921/20.

XX Targeted delivery system comprising a bioactive agent homogeneously  
 XX dispersed in a targeted matrix is especially useful in cancer therapy

XX Disclosure; Page14; 46pp; English.

XX The invention relates to a composition comprising a bioactive agent  
 XX homogeneously dispersed in a targeted matrix (polymer and targeting  
 XX ligand). Also included are a targeted matrix for use as a delivery  
 XX vehicle comprising a polymer associated with a targeting ligand,  
 XX enhancing the bioavailability of an agent comprising administration of the  
 XX of the composition and treating cancer comprising administration of the  
 XX novel composition. The method is useful for targeted delivery of a drug,  
 XX especially in cancer therapy. The targeting ligand may be a peptide.  
 XX Examples of targeting peptides are disclosed including cathepsin-D  
 XX substrate peptides, peptides targeting receptors in the brain and  
 XX kidney, peptides recognising fibronectin- and vitronectin-binding  
 XX integrins, peptides targeting the RGD (Arg-Gly-Asp)-motif in, e.g.,  
 XX antibodies, peptides targeting the angiogenic endothelium of solid

CC tumours, tissue specific peptides (e.g. of lung, skin, pancreas,  
 CC intestine, uterus, adrenal gland and retina), and cationic cancer-  
 CC targeting peptides. The present sequence is a peptide targeting  
 CC ligand disclosed in the invention.

XX

SQ Sequence 32 AA;

Query Match

Best Local Similarity 77.7%; Score 99.5; DB 24; Length 32;

Matches 22; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

OY 2 VLKIGTVALHAGKALGAVDTISQ 27

Db 6 MLKIGTVALHAGKALGAVDTISQ 30

Search completed: December 10, 2003, 20:27:42

Job time : 42 secs